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OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                         Dytabase :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perfect score:
     April 15, 2003, 12:01:27; Search time 131 Seconds (without alignments) 189.942 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-017-372E-37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                         Published_Applications_AA:*
: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
    /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
    /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
    /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
    /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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    /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
    /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
    /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

19	18	17	16	15	14	13	12	11	10	9	8	7	6	₅	4	ω	2	_	Result No.
824.5	826.5	827.5	834	868	868.5	871.5	1047	1139	1262.5	1572.5	1835.5	1835.5	1893.5	1905.5	1909	1914.5	1929.5	2030.5	Score
38.2	38.3	38.3	38.6	40.2	40.2	40.4	48.5	52.8	58.5	72.8	85.0	85.0	87.7	88.3	88.4	88.7	89.4	94.0	Query Match Length DB
412	412	410	409	383	382	412	373	447	455	315	390	390	390	390	391	390	390	390	ength
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US-09-214-592-19	US-09-214-592-24	US-09-214-592-22	US-09-214-592-27	US-09-756-283A-27	US-09-214-592-34	US-09-214-592-31	US-09-214-592-32	US-09-756-283A-22	US-09-756-283A-20	US-09-214-592-25	US-09-214-592-23	US-09-214-592-20	US-09-214-592-28	US-09-756-283A-23	US-09-214-592-17	US-09-214-592-33	US-09-214-592-29	US-09-214-592-26	ID
Sequence 19, Appl	Sequence 24, Appl	Sequence 22, Appl	Sequence 27, Appl		Sequence 34, Appl			Sequence 22, Appl	Sequence 20, Appi	Sequence 25, Appl	Sequence 23, Appl	Sequence 20, Appl	28,			ر ا ا ا	, 60	Sequence 26, Appl	Description

45	44	43	42	41	40	39	38	37	36	35	34	3 3	32	31	30	29	28	27	26	25	24	23	22	21	20
482	482	493	500	500	500	500	500	504	504	535	542	638	638	638	638	638	638	753.5	792	808	809	809	820.5	824	824.5
22.3	22.3	22.8	23.2	23.2	23.2	23.2	23.2	23.3	23.3	24.8	25.1	29.6	29.6	29.6	29.6	29.6	29.6	34.9	36.7	37.4	37.5	37.5	38.0	38.2	38.2
113	112	115	115	114	114	113	112	114	112	112	116	115	115	114	114	113	112	139	304	412	414	414	412	414	412
٤	10	9	9	12	10	9	10	12	10	10	12	ဖ	9	12	10	9	10	12	10	9	10	9	10	9	12
US-09-813-398-14	US-09-813-271B-4	US-09-859-211-49	US-09-880-708-27	US-10-115-406-23	US-09-813-459-24	US-09-813-398-15	US-09-813-271B-6	US-10-115-406-25	US-09-813-271B-12	US-09-813-271B-8	US-10-115-406-24	US-09-880-708-25	US-09-859-211-47	US-10-115-406-21	US-09-813-459-22	US-09-813-398-13	US-09-813-271B-2	US-10-002-278-8	US-09-756-283A-26	US-09-214-592-30	US-09-756-283A-24	US-09-214-592-18	US-09-756-283A-25	US-09-214-592-21	US-10-028-158-21
seducince ta, white	1 4	· (c		2 6	4 0	-		١,٢	Sequence 12, Appl	Sequence 8, Appli	Sequence 24, Appr	Sequence 25, Appr	4,	. 12.	Sequence 22, Appl	بار		ά	•	Sequence 30, Appr	~	Ò	, ,		21,

ALIGNMENTS

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RESULT 1
US-09-214-592-26
; Sequence 26, Application US/09214592A
; Publication No. US20030027218A1
; Publication No. US20030027218A1
; GENERAL INFORMATION:
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; LENGTH: 390
; TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Yamasaki,CMotoo
APPLICANT: Shibata,CKenji
APPLICANT: Sato,CYasufumi
TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND METHOD
TITLE OF INVENTION: OF SCREENING TGF- ACTIVITY-REGULATING COMPOUNDS
FILE REFERENCE: 11060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/214,592A CURRENT FILING DATE: 1999-01-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
                                                                                                                          181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIBGFRLSAHSSSDSKDNTLHVEINGFN 240
241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNSYPYDVPDYASLALDTN 300
                                                                                                                                                                                                              61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMLESGNQI 120
                                                                                                                                                                                                                                     61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
                                                                                                                                                                                                                                                                                                                                                                                 v Match 94.0%;
Local Similarity 94.8%;
nes 386; Conservative
                                                                                                                                                                                                                                                                                                 1 MPPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
                                                                                                                                                                                                                                                                                                                     1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
                                                                                                                                                                                                                                                                                                                                                                                 Score 2030.5; DB 9; Length 390;
Pred. No. 9e-165;
1; Mismatches 3; Indels 17;
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RESULT 3
US-09-214-592-33
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LENGTH: 390
TYPE: PRT
                                        Sequence 33, Application US/09214592A Publication No. US20030027218A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 29, Application US/09214592A Publication No. US20030027218A1
APPLICANT: Yamasaki,CMotoo
APPLICANT: Shibata,CKenji
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CURRENT FILING DATE: 1999-01-18
NUMBER OF SEQ ID NOS: 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Yamasaki,CMotoo
APPLICANT: Shibata,CKenji
APPLICANT: Sato,CYasufumi
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                                                                                                                                                                                                      361 NQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 YDKMKSSSHSIYMFFNTSELREAVPEPVLLSRADVRLLRLKLKVEQHVELYQKYSNNSWR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MPPSGLRLLPLLLPLLWLLMLTPGRPVAGLSTCKTIDMELVKRKGIEAIRGQILSKLRLA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
                                                                                                                                                                                                                                                                                      YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY 360
                                                                                                                                                                                                                                                                                                                                                                   SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNSYPYDVPDYASLALDTN 300
                                                                                                                                                                                 NQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
                                                                                                                                                                                                                                                                                                                                               SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRR-----ALDTN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89.4%; score 1929.5; DB 9; Length 390; 89.7%; Pred. No. 3.5e-156;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180
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; ORGANISM: human US-09-214-592-17
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        Matches
                                                                                                                                                                        SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                          Best
                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 33
LENGTH: 390
                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/214,592A CURRENT FILING DATE: 1999-01-18
                                                                                                                                                                                                                                                                             APPLICANT: Yamasaki,CMotoo
APPLICANT: Shibata,CKenji
APPLICANT: Sato,CYasufumi
TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND METHOD
TITLE OF INVENTION: OF SCREENING TGF- ACTIVITY-REGULATING COMPOUNDS
FILE REFERENCE: 11060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                SOFTWARE:
                                                                                                                                                                                                                    NUMBER OF SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Sato, CYasufumi
TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF-
TITLE OF INVENTION: OF SCREENING TGF- ACTIVITY-REGULATING COMPOUNDS
FILE REFERENCE: 11100
                                                                                                                                LENGTH: 39
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/214,592A CURRENT FILING DATE: 1999-01-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 34
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TYPE: PRT
      hes 365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 NQHNPGASAAPCCVPQALEPLPIVYYYGRKPKVEQLSNMIVRSCKCS 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       344 NQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       284 YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR-------ALDTN 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
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                        Similarity
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    Conservative
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88.4%; Score 1909; DB 9;
89.5%; Pred. No. 1.9e-154;
tive 10; Mismatches 15;
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89.4%;
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Gaps
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1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60

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US-09-756-283A-23
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APPLICANT: Chernajovsky, Yuti
APPLICANT: Dreja, Hanna Stina
APPLICANT: Adams, Gillian
TITLE OF INVENTION: Latent Fusion Protein
FILE REFERENCE: 0623.1000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 23, Application US/09756283A Patent No. US20020151478A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 23
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 88.3%; Score 1905.5; DB 10; Length 390; Best Local Similarity 89.2%; Pred. No. 3.8e-154;
                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                          ; Sequence 20, Application US/09214592A ; publication No. US20030027218A1 ; GENERAL INFORMATION:
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US-09-214-592-20
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LENGTH: 390
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APPLICANT: Shibata,CKenji
APPLICANT: Sato,CYasufumi
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TITLE OF INVENTION: OF SCREENING TGF- ACTIVITY-REGULATING COMPOUNDS
FILE REFERENCE: 11060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/214,592A CURRENT FILING DATE: 1999-01-18
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              APPLICANT: Yamasaki,CMotoo
APPLICANT: Shibata,CXenji
APPLICANT: Shibata,CXenji
APPLICANT: Sato,CYasufumi
TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF-
TITLE OF INVENTION: OF SCREENING TGF- ACTIVITY-REGULATING COMPOUNDS
FILE REFERENCE:
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; ORGANISM: rat
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                                                                                                                                                                                                                                                                                                                    Sequence 23, Application US/09214592A
Publication No. US20030027218A1
GENERAL INFORMATION:
APPLICANT: Yamasaki,CMotoo
APPLICANT: Shibata,CKenji
APPLICANT: Shibata,CKenji
APPLICANT: Sato,CYasufumi
TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF-
TITLE OF INVENTION: OF SCREENING TGF- ACTIVITY-REGULATING COMPOUNDS
FILE REPERENCE: 11060
                                                                                                       Matches
                                                                                                                                       Query Match
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Best Local Similarity
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LENGTH: 390
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                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 34
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                                                 1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
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                                MPPSGLRLLPLLPLPWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
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                                                                                                  85.0%; Score 1835.5; DB 9; 85.0%; Pred. No. 3.4e-148; tive 14; Mismatches 30;
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Pred. No. 3.4e-148;
5; Mismatches 29; Indels 17;
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US-09-214-592-25
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; Publication No. US20030027218A1
; GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/214,592A CURRENT FILING DATE: 1999-01-18
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APPLICANT: Shibata,CKenji
APPLICANT: Sato,CYasufumi
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TYPE: PRT
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                                      376
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 284 QALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS
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                                    QALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 407
                                                                       YIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVP
                                                                                      YIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVP
                                                                                                                                                PFLLLMATPLERAQHLHSSRHRR-
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88.9%;
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RESULT 10
US-09-756-283A-20
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APPLICANT: Dreja, Hanna Stina
APPLICANT: Dreja, Hanna Stina
APPLICANT: Adams, Gillian
TITLE OF INVENTION: Latent Fusion Protein
FILE REFERENCE: 0623,1000000
CURRENT APPLICATION NUMBER: US/09/756,283A
CURRENT FILLING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 100
SOFTWARE: PatentIn version 3.0
SEQ ID NO 22
LENGTH: 447
TYPE: PRT
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US-09-756-283A-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20, Application US/09756283A Patent No. US20020151478A1 GENERAL INFORMATION:
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APPLICANT: Dreja, Hanna Stina
APPLICANT: Adams, Gillian
TITLE OF INVENTION: Latent Fusion Protein
FILE REFERENCE: 0623.1000000
                                   Query Match
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                                                                                         OTHER INFORMATION: mIFN -LAP construct
                                                                                                         ORGANISM: Artificial Sequence FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLL-RLKLKVEQHVELYQKYSNDSW 179
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Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58.5%; score 1262.5; DB 10; Length 455; 90.5%; Pred. No. 2.3e-99;
 52.8%; Score 1139; DB 10; 87.0%; Pred. No. 7.1e-89; tive 10; Mismatches 18;
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                                     Length 447;
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SEQ ID NO 32
LENGTH: 373
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APPLICANT: Shibata,CMotoo
APPLICANT: Shibata,CMos)i
APPLICANT: Sato,Cyasufumi
TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF-
TITLE OF INVENTION: OF SCREENING TGF- ACTIVITY-REGULATING COMPOUNDS
TITLE OF INVENTION: OF SCREENING TGF- ACTIVITY-REGULATING COMPOUNDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       426 GMNRPFLLLMATPLERAQHLQS 447
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                                                                                                                                                                                                                                                                                                         121 LLHRAELRMLRQKAAADSAGTEQRLELYQGYGNASWRYLHGRSVRATADDEWLSFDVTDA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73 LPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQIYDKFKGTPHSLY 132
                   377 ALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GMNRPFLLLMATPLERAQHLHS 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFTTGRRGDLATIH
                                                                                                                                                                             LLMATPLERAQHLHSSRHRRALDINSYPYDVPDYASLALDINYCF--SSTEKNCCVRQLY 316
                                                                                                                                                                                                                       VHQWLSGSELLGVFKLSVHCPCEMGPGHAEEMRISIEGFEQ-QRGDMQSIAKKHRRVPYV 239
                                                                                                                                                                                                                                                              VROWLTRREAIEGFRLSAHSSSD---SKDNTLHVEINGFNSGRRGDLATIHGMNR--PFL 258
                                                                                                                                                                                                                                                                                                                                           LLSRAELRLLRLKLK-----VEQHVELYQKYSNDSWRYLSNRLLAPSDSPEWLSFDVTGV 203
                                                                                                                                                                                                                                                                                                                                                                                        QRARLRPPPDGPDEYWAKELRRIPMETTWDGAMEHWQPQSHSIFFVFNVSRARRG-GRPT 120
                                                                                                                                                                                                                                                                                                                                                                                                                              GES-VEPEPEPEADYYAKEVTRVLMVESGNQIYDKFKGTPHSLYMLFNTSELREAVPEPV 148
                                                   IDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQ
                                                                                                                                          LAMALPAERANELHSARRRR------
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h 48.5%; Score 1047; DB 9; Length 373; Similarity 52.9%; Pred. No. 3.7e-81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52; Mismatches 100;
                                                                                                                                               -----DLDTDYCFGPGTDEKNCCVRPLY
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US-09-214-592-34
; Sequence 34, Application US/09214592A
; Publication No. US20030027218A1
; GENERAL INFORMATION:
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Publication No. US20030027218A1
GENERAL INFORMATION:
                            TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND METHOD TITLE OF INVENTION: OF SCREENING TGF- ACTIVITY-REGULATING COMPOUNDS FILE REFERENCE: 11060
        CURRENT APPLICATION NUMBER: US/09/214,592A
                                                                                 APPLICANT: Yamasaki,CMotoo
APPLICANT: Shibata,CKenji
APPLICANT: Sato,CYasufumi
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CURRENT FILING DATE: 1999-01-18
NUMBER OF SEQ ID NOS: 34
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APPLICANT: Shibata, CKenji
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 AKQRYLSGRNVQTRGSPEWLSFDVTDTVREWLLHRESNLGLEISIHCPCHTFQPNGDILE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125 KGVTSNVFR-FNVS---SAEKNSTNLFRAEFRVLRVPNPSSKRSEQRIELFQILRPDEHI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 KGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL----KLKVEQHVELYQKYSND--- 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 YQILALYNSTRELL--EEMEEEKEESCSQENTESEYYAKEIHKFDMIQGLPEHNELGICP 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75 EAVLALYNSTRDRVAGESVEPEPE-----PEADYYAKEVTRVLMVE---SGNQIYDKF 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                 ------ALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYFANF 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -SWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAH-----SSSDSKD 229
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; ORGANISM: Rana sp. US-09-756-283A-27
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US-09-214-592-34
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SEQ ID NO 27
LENCTH: 383
TYPE: PRT
                                                                                                                                                                                                                                                               Query Match
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SEQ ID NO 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/756,283A CURRENT FILING DATE: 2001-01-09 NUMBER OF SEQ ID NOS: 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Dreja, Hanna Stina
APPLICANT: Adams, Gillian
TITLE OF INVENTION: Latent Fusion Protein
FILE REFERENCE: 0623.1000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Chernajovsky, ruti
APPLICANT: Dreja, Hanna Stina
APPLICANT: Adams, Gillian
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Best Local Similarity
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          271 --GVGQEYCFGNNGPNCCVKPLYINFRKDLGWKWIHEPKGYEANYCLGNCPYIWSMDTQY 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          294 SLALDTNYCFSSTEKNCCVROLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQY 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       236 INGFNSGRRGDLATIHGM--NRPFLLLMATPLERAQHLHSSRHRRALDINSYPYDVPDYA 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            171 SRYLESKYITPVTDDEWMSFDVTKTVNEWLKRAEENEQFGLQPACKCPTPQAKD----ID 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 -----HEFKFKFNASHVRENVGMNSLLHHAELRMYKKQTDKNMDQRMELFWKYQENGTTH 170
60 EKMTVPSEAIFLYNSTLEVIREKATREEEEHVGHDQNIQDYYAKQVYR---FESITELED 116
                                                  69 PPGPLPEAVLALYNSTRDRVAGESVEPEPEPEA-----DYYAKEVTRVLMVESGNQIYD 122
                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 -RYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAH---SSSDSKDNTLHVE 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 FKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKL--KVEQHVELYQKYSNDSW-- 179
                                                                                                  1 MEVLWMLLVLLVLHLSSLAMSLSTCKAVDMEEVRKRRIEAIRGQILSKLKLDKIPDV-DS 59
                                                                                                                                                  9 LPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDV 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 PPGPLPEAVLALYNSTRDRVAGESVEPE-----PEPEADYYAKEVTRVLMVESGNQIYDK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 LPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDV 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MEVLWMLLVLHLSSLAMSLSTCKAVDMEEVRKRRIEAIRGQILSKLKLDKTPDV-DS 59
                                                                                                                                                                                                               191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IEGF-PALRGDLASLSSKENTKPYLMITSMPAERIDTVTSSRKKR-------
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                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                     40.2%; Score 868; DB 10;
46.0%; Pred. No. 6.4e-66;
ative 54; Mismatches 122;
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Search completed: April 15, 2003, 12:04:3 Job time : 134 secs

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2159
1 MAPSGLRLLPLLLPLLWLLV......GRKPKVEQLSNMIVRSCKCS 407
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Match
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Gapop 10.0 , Gapext 0.5
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Q91VP5
Q91449
Q9PTQ2
Q9ERB7
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                    Q9tum8 equus cabal
Q8r4d9 sigmodon hi
Q91yu7 mus musculu
Q9pwa9 morone chry
Q91vp5 mus musculu
Q9ptq2 cyprinus ca
Q9ptq7 mesocricetu
Q9pk17 mus musculu
Q99k17 mus musculu
Q99k17 mosocricetu
Q99k17 mosocricetu
Q99k17 mus musculu
Q95n80 canis famil
Q98854 cyprinus ca
Q921t1 mus musculu
Q951t1 mus musculu
Q95t08 canis famil
                                                                                                                                                                                                                                                                                                                                                                                 Description
Q90yf1 pleuronecte
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scopht	Q9DEP5	13	62	13.3	287	45
Q98tb3 morone chry	Q98TB3	13	377	13.3	287.5	44
oncorhy	Q90ZD1	13	373		38	3
Q90w05 sparus aura	Q90W05	13	385		294	42
Q90w06 umbrina cir	Q90W06	13	376		294	41
Q98tb4 oreochromis	Q98TB4	13	376		295	40
	Q8WNS6	6	375	13.7	296.5	39
	Q90YF4	13	62	ω	300	38
	Q90ZJ7	13	62	ω.	301	37
ervus	Q28240	6	50	4.	302	36
Q95j86 macaca fasc	Q95J86	6	375		90	ω 5
anser	Q8UWD9	13	375	4	311.5	34
Q8uwe0 anas platyr	Q8UWE0	13	375		13	ω
Q9gm97 equus cabal	Q9GM97	σ	375		313.5	32
	Q98SP0	13	375	4.	316.5	31
oncorhynch	Q90YF8	13	77	4	317	30
Q90yy0 ictalurus p	Q90YY0	13	389	4	N)	29
Q8uwd7 coturnix ch	Q8UWD7	13	375	٠	321.5	28
8p	Q8UWD8	13	375	ū	w	27
	Q9N1S3	σ	81	σ,	358	26
Q8wv88 homo sapien	Q8WVB8	4	309	7.	371.5	25
	Q28241	σ	86	7.	373	24
	Q9MYZ1	σ	91	7.	383	23
	042306	13	87	•	393	22
	Q90ZE7	Ľ	88	18.4	397	21
_	Q90YF7	13	88	8	402	20
	Q90YF5	13	88	9	413	19
0yf2 pleuronec	Q90YF2	13	179	21.1	456	18
Q9r184 meriones un	Q9R184	11	101		554	17

ALIGNMENTS

X B Q	RESULTION A CO	
Query Match Best Local : Matches 34	JUT 1 JUM QTUM8 QOTUM8; QOTUM8; QOTUM8; QOTUM8; QOTUM9; QOTUM-2 1 ransfor TGFB1. Equus ca Eukaryot Mammalia ROBL_Tax SEQUUNCE Nixon A. "Molecul a diverg peptide Submitte -!-SIMI EMBL; AF HSSP; PO InterPro In	
itch Sal Sim	T 1 Q9TUM8 Q9TUM8; Q1-MAY-2000 (TrE Q1-MAY-2000 (TrE Q1-UN-2002 (TRE Q1-UN-20	
Query Match Best Local Similarity 85. Matches 348; Conservative	T 1 Q9TUM8 Q9TUM8; PRELIMINARY; PRT; 390 AA. Q9TUM8; Q1-MAY-2000 (TrEMBLrel. 13, Created) Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update) Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update) Transforming growth factor beta 1. TGFB1. Equus caballus (Horse). Equis Eutheria; Perissodactyla; Equidae; Equidae; Eutharyota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Perissodactyla; Equidae; Equus. NCBTaxID-9796; [1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. Mixon A.J., Brower-Toland B.T., Sandell L.J.; Nixon A.J., Brower-Toland B.T., S	
84.1%; 85.5%; vative	PRELIMINARY; PRT; (TTEMBLICAL 13, Create (TTEMBLICAL 13, Last a (TTEMBLICAL 21, Last a GIVEMBLICAL CIAN US (HOTSE). When A 1. M N. A. STORAGE STRUCTURE THE MEMBLIG GIVEMBLIGHT TOFF OFF AAD49431.1; FROM 139; TGFD N FROM 111; TGF	
12	PRT; 390 AA. 13, Created) 13, Last sequence updat 21, Last annotation upd tor beta 1. rdata; Craniata; Vertebr issodactyla; Equidae; Eq ind B.T., Sandell L.J.; quine transforming growt structure that encodes a species."; puncture that encodes a the EMBL/GenBank/DDBJ d TO THE TGF-BETA FAMILY. 1.1; 1.1; 2.1 2.1 2.1 2.1 2.1 2.1 3.1 4.1 5.1 5.1 5.1 5.1 5.1 5.1 5.1 5.1 5.1 5	
ore 1815.5; ed. No. 3.1 Mismatches	ted) seque annot 1. aniata la; Ec la	
Score 1815.5; DB 6 Pred. No. 3.1e-149; ; Mismatches 30;	ated) t sequence update t annotation upda 1. Sandell L.J.; ansforming growth e that encodes a : ", TGF-BETA FAMILY. 220FE40DFCCA6016	
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Best Local S
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Transforming growth factor beta-1 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sigmodon
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Blanco J.C., Pletneva L.M., Prince G.A.; "Cotton rat cytokines, chemckines, and interferons."; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases EMBL; AF480858; AAL87199.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                             AVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWRYLSNRLLAPSDSPEWLSFDVTG
                                                                                                                                                                                                                                                               NQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 407
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                                                        VVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFNSGRRGDLATIHGMNRPFLLLMA 262
                                                                                                               AVPEPPLLSRAELRLQRFKSNVEQHVELYEKYSNNSWRYLGNRLLSPTDSPEWLSFDVTS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NQHNPGASAAPCCVPQVLEPLPIVYYVGRKPKVEQLSNMIVRSCKCS
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                                       VVRKWLNQGDGIQGFRFSAHCSCDSKDNILHVEINGISPKRRGDLGTIHDMNRPFLLLMA
                                                                                                                                                                                      STRDRVAGESADPEPEPEADYYAKEVTRVLMVDRNNAIYDKTKDIPHSVYMFFNTSDIRE
                                                                                                                                                                                                          STRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQIYDKFKGTPHSLYMLFNTSELRE
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84.4%; Pred. No. 2e-1
tive 16; Mismatches
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NO. 2e-142;
Thes 27;
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O91YU7;

Q91YU7;

Q91YU7;

Q1-DEC-2001 (TrEMBLrel. 19, Created)

O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)

O1-UN-2002 (TrEMBLrel. 21, Last annotation updat

"ransforming growth factor, beta 3."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPRO01839; TGFb_N.
InterPro; IPRO01111; TGFb_N.
Pfam; PF000019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1.
ProDom; PD000357; TGF_BETA_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases -:- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; BC014690; AAH14690.1; MGD; MGI:98727; Tgfb3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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348
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                                                 343 CPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVR 402
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CPYLRSADTTHSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVK
                                                                                                                                       NSYPYDVPDYASLALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGP
                                                                                                                                                                                                                                                                            --TLHVEINGFNS---GRRGDLATIHGM---NRPFLLLMATPLERAQHLHSSRHRRALDT
                                                                                                                                                                                                                                                                                                                                   QRYIGGKNLPTRGTAEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNGDILENV
                                                                                                                                                                                                                                                                                                                                                                  WRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAH------SSSDSKDN-
                                                                                                                                                                                                                                                                                                                                                                                                                                             ITSKVFR-FNVSSVEK----NGTNLFRAEFRVLRVPNPSSKRTEQRIELFQILRPDEHIAK 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YQVLALYNSTRELLEEMHGEREEGCTQETSESEYYAKEIHKFDMIQGLAEHNELAVCPKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EAVLALYNSTR----DRVAGESVE--PEPEPEADYYAKEVTRVLMVE---SGNQIYDKFKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LVVLALLNLATISLSTCTTLDFGHIKKKRVEAIRGQILSKLRLTSPPEPSVMT--HVP
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                                                                                                                                                                                                                     HEVMEIKFKGVDNEDDHGRGDLGRLKKQKDHHNPHLILMMIPPHRLDSPGQGSQRK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL----KLKVEQHVELYQKYSND----S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           412 AA; 47144 MW; F3EB65D046DF32AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                       KRALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38.3%; Score 827.5; DB 1
44.2%; Pred. No. 1.9e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57; Mismatches 127; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vert
Sciurognathi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 11; Length
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PROBLEM OF THE TENT OF THE TEN
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RE FISH Shellfish Immunol. 10:61-85(2000).

C :- FUNCTION: IS LIKELY TO BE AN IMPORTANT CYTOKINE REGULATING IMMUNE RESPONSE. MAY ALSO HAVE A ROLE IN OTHER PHYSIOLOGICAL SYSTEMS.

C :- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).

C :- TISSUE SPECIFICITY: HIGHER LEVELS FOUND IN MONONCILEAR CELLS FROM DERIPHERAL BLOOD THAN IN SPLEEN OR ANTERIOR KIDNEY.

C :- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

DR EMBL; AF140363; AAD46997.1; -.

R HSSP; P01137; IKLA.

DR Ffam; PF000189; TGFb_Dropeptide; 1.

PR Pfam; PF00688; TGFb_propeptide; 1.

PR PFAM; PD000357; TGFb; 1.

PR PFAM; PD000357; TGFb; 1.
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                                                                                                                                        Q
                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                           Query Match
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Transforming growth factor beta precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID DISULFID DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9PWA9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tompkins W.A.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Harms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20394636; PubMed=10938723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSOMEXIONEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=45352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Growth factor; Mitogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00204; TGFB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Cloning and sequencing hybrid striped bass (Morone saxatilis x M
                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
                                 72
                                                                                                                                              15 LLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRL---ASPPSQGDVPPG
                                                                                                                                                                                                                                   Local
                                                                                       6
PLPEAVLALYNSTRDRVAGESVEPE-----PEPEADYYAKEVTRVLMVESGNQIYDKFKG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C.A., Kennedy-Stoskopf S., Horne W.A., Fuller F.J.,
                                                                                       LMLVVVYTVGN-VSGMSTCKTLDLEMVKKKRIEAIRSQILSKLRLFKEPEPDQAGDEEEI 64
                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS00250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                       382 AA;
                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGF_BETA_1;
                                                                                                                                                                                                                                                                                                                                                                           108
113
124
259
                                                                                                                                                                                                                                                                                                                       43846 MW;
                                                                                                                                                                                                                                   38.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycoprotein; Signal
                                                                                                                                                                                                          65;
                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. . .) (PÓTENTIAL).

"-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                   Score 825; DB 13; Pred. No. 2.8e-63;
                                                                                                                                                                                                                                                                                                                                                      CELL ATTACHMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSFORMING GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                          3124D8C34EA74D72 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY.
                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 382 AA
                                                                                                                                                                                                             108;
                                                                                                                                                                                                                                                                                                                                                      SITE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FACTOR BETA.
                                                                                                                                                                                                                                                              Length 382;
                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                             15;
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RESULT 5
091VP5
ID 091V
AC 091
                                                        Ω
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                                                                                                                                                                                      QΥ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       091VP5;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
Similar to transforming growth factor, beta 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:98726; Tgfb2.
InterPro; IPR0011839; TGFb.
InterPro; IPR001111; TGFb_N.
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_Propeptide;
ProDom; PD000357; TGFb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Mus musculus (Mouse).
Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. -:- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q91VP5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein.
SEQUENCE 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prodom; pD000357; TGFb; 1.
proSITE; pS00250; TGF_BETA_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=BREAST TUMOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 PTP--LLSLYNSTKEMLKEQQTEVQTDISTEQEEEEYFAKVLHKFNMTRKNN------
                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                      Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G-RGDTGPMQLLTQQPPYILTMSIP----QNISSPSTSRKKRSTETK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RFITNKWKDKWLSFDVTKTLQDWLKGTDDEQGFQLRLFCECNKVSAGETIFKFGISGIDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGF--RLSAHSSSDSKDNTL-HVEINGFNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKV--EQHVELYQKYSNDSWRYLSN 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---DVCTAQTE-TCCVRSLYIDFRKDLGWKWIHKPTGYNANYCMGSCTYIWNAENKYSQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GRRGDLATIHGMNR---PFLLLMATPLERAQHLHS---SRHRRALDINSYPYDVPDYASLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TDTTKKMFFNISEIRESVGDYRLLTSAELRMLIKKTTIYDEQRVELYSGL-GDSPRYLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKV 356
LTSPTQRYIDSKVVKTRAEGEWLSFDVTDAVQEWLHHKDRNLGFKISLHCPCCTFVPSNN
                                                                                                                                                                                          KFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL---KLKV-EQHVELYQ-----K 173
                                                                                                                                                                                                                                                                                                                                                                                               VLSTFLLLHLVP--VALSLSTCSTLDMDQFMRKRIEAIRGQILSKLKLTSPPE--DYPEP 60
                                                               YSNDSWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSS---
                                                                                                                                                                                                                                                                                                                            GPLPEAVLALYNSTRD----RVAGESVEPEPE-PEADYYAKEVTRVLM---VESGNQIYD 122
                                                                                                                                                                                                                                                                    DEVPPEVISIYNSTRDLLQEKASRRAAACERERSDEEYYAKEVYKIDMPSHLPSENAIPP
                                                                                                                                  TFY-RPYFRIVRFDVSTMEKNASN---LVKAEFRVFRLQNPKARVAEQRIELYQILKSKD 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BC011170; AAH11170.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          414 AA; 47588 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38.0%; Score 821; DB 11;
43.3%; Pred. No. 7.1e-63;
tive 62; Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB37A7C38881F286 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                              120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15;
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14;

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RESULT 093449

AC 09409

AC 099449

AC 099449

AC 099449

AC 099449

AC 0997

AC 099
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                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    analysis reveals tissue specific expression and a potential regulatory sequence in rainbow trout (Oncorhynchus mykiss).";

Cytokine 10:555-563(1998).
                                                                                                                            Growth factor; Mitogen; Glycoprotein;
                                                                                                                                                          PROSITE; PS00250; TGF_BETA_1; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=LEUKOCYTE;
MEDLINE=98390168; PubMed=9722928;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99242020; PubMed=10227481;
Daniels G.D., Secombes C.J.;
"Genomic organisation of rainbow trout, Oncorhynchus mykiss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
NCBI_TaxID=8022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        093449; 091217;
01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence
01-JUN-2002 (TrEMBLrel. 21, Last annotatic
Transforming growth factor beta precursor.
TGF-BETA OR TGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hardie L.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-LEUKOCYTE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  093449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  401
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                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: IS LIKELY TO BE AN IMPORTANT CYTOKINE REGULATING IMMUNE RESPONSE. MAY ALSO HAVE A ROLE IN OTHER PHYSIOLOGICAL SYSTEMS. SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY). TISSUE SPECIFICITY: EXPRESSED IN BLOOD LEUKOCYTES, KIDNEY MACROPHAGES, BRAIN, GILL AND SPLEEN BUT NOT IN LIVER. SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Comp. Immunol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vanecagacpylmssdfQftkvlslyntinpeasaspccvsQdleplfilyyiGnfpki 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---DSKDNTLHVE---INGFNSGRRGDLATIHGMNR-----PFLLLMATPLERAQHLHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EQLSNMIVKSCKCS 414
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21, Last annotation update)
TRANSFORMING GROWTH FACTOR BETA BY SIMILARITY. BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9PTQ2 PRELIMINARY; PRT; 376 AA. Q9PTQ2; Q1-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Transforming growth factor beta precursor.
                                                                                                                                                    "Molecular cloning of carp transforming growth factor beta 1.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: IS LIKELY TO BE AN INFORTANT CYTOKINE REGULATING IMMUNE RESPONSE. MAY ALSO HAVE A ROLE IN OTHER PHYSICIOGICAL SYSTEMS.
-!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
-!- SUBUNIT: BELONGS TO THE TGF-BETA FAMILY.
                                                         InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb_N.
                                                                                                              EMBL; AF136947; AAF22573.1; HSSP; P01137; 1KLA.
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. Yin Z., Kuang J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
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CONFLICT
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                              TGF-beta;
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Pred. No. 1.3e-61;
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-> D (IN REF. 2).
N-> D (IN REF. 2).
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93BD4D3540084B92 CRC64;
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O9ERB7;
O1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
O1-MAR-2002 (TrEMBLrel. 21, Last annotation update)
Transforming growth factor-beta 2 (Fragment).
Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Cricetinae;
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Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
EMBL; AY007214; AAG02247.1; -.
HSSP; P08112; 2TGI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9ERB7
                                                                                                   cycle."
                                                                                                                             growth factor-beta isoforms
                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                     Ramesh G., Kondaiah P., Seshagiri P.B.;
"Differential expression and selective localization of transforming
                                                                                                                                                                                                                                                      NCBI_TaxID=10036;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VLALYKHHNPGASAQPCRVPQVLNPLPIFYYVGRQHKVEQLSNMIVKTCKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KS-RYLESRFI--PNQRKWLSFDVTQTLKDWLQRSEAEQGFQLKMADNCDPQ-KTFQLKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---DKF-----LWFNITDISQTLGLNRIISQVELRLLITTFPDGSEQRLELYQVIGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QIYDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLK--VEQHVELYQKYSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDVPPGP-LPEAVLALYNST---RDRVAGESVEPEPEP-EADYYAKEVTR--VLMVESGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALDTNYCFSSTEKNCCVROLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSK 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGLVL-VRGDTETLAVNMPRPHILVMSLPLD-GNNSSKSRRKRQTETDQVCTDKSD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NGFNSGRRGDLATIH-GMNRPFLLLMATPLERAQHLHSSRHRRALDTNSYPYDVPDYASL
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43.6%;
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BY SIMILARITY.
BY SIMILARITY.
EX SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
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                                                                                                                                in the hamster uterus
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Pred. No. 2.
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.2e-59;
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                      HSSP; P10600; 1TGJ.

MGD; MGI:98727; Tgfb3.

InterPro; IPR001839; TGFb.

InterPro; IPR0013111; TGFb.N.

InterPro; IPR003911; TGF_TGFb.

Pfam; PF00019; TGF_beta; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q99K17
Q99K17;
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InterPro; IPR001111; TGFb_N.
                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                   Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases
-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to transforming growth factor, beta 3 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGFB3
                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VLALYNSTRD----RVAGESVEPEPE-PEADYYAKEVTRVLM---VESGNQIYDKFKGTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGACPYLWSSDTQHTKVLSLYNTINPEASASPCCVSHDLEPLTILYYIGNTPKIEQLSNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNTLHVE---INGFNSGRRGDLATIHGMNR-----PFLLLMATPLERAQHLHSSRHRRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSLYMLFNTSELREAVPEPVLLSRAELRLLRL---KLKV-EQHVELYQ-----KYSNDSW 179
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177; Conser
     PF00688;
                                                                                                                                                                                     BC005513; AAH05513.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----ALDAAYCFRNVQDNCCLRPLYIDFKRDLGWKWIHEPKGYNANFC
  TGFb_propeptide;
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                                                                                                                                                                                                                                                                                                                                                                        Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35.2%; Score 760;
42.1%; Pred. No. 1
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1.3e-57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62;
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                                                                                                                                                                                                                                                   STRAIN-LVG (SYR);

MEDLINE-93304479; PubMed-8317544;

Wong D.T., Donoff R.B., Yang J., Song B.Z., Matossian K., Nagura N.,

Elovic A., McBride J., Gallagher G., Todd R.;

"Sequential expression of transforming growth factors alpha and beta
by eosinophils during cutaneous wound healing in the hamster.";

Am. J. Pathol. 143:130-142(1993).
                                                    MEDLINE-98234044; PubMed-9573100;
Melby P.C., Tryon V.V., Chandrasekar B., Freeman G.L.;
"Cloning of Syrian hamster (Mesocricetus auratus) cyto
analysis of cytokine mRNA expression in experimental v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       008714 PRELIMINARY; PRT; 130 AA. (008714, 070331; 0708714, 070331); 01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Transforming growth factor beta 1 (TGF-beta 1) (Fragment). TGFB1.
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                                                                                                                                                                            STRAIN-SYRIAN; TISSUE-SPLEEN;
                                                                                                                                                                                                           SEQUENCE OF 26-115 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
      infect. Immun.
                                 eishmaniasis."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mesocricetus auratus (Golden hamster).
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66:2135-2142(1998).
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                                                                                      cytokine cDNAs
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                                                                                                                                                                                                                                                                                                    Q95N80;
   SEQUENCE
                                    Glycoprotein.
                                                                                    -1- SIMILARITY: BELONGS TO THE EMBL; AF349538; AAK54072.1; -. InterPro; IPR001839; TGFb.
                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                 PROSITE; PS00250; TGF_BETA_1;
                                                              ProDom; PD000357;
                                                                         Pfam; PF00019; TGF-beta;
                                                                                                                                              Fonfara S., Groene A., Baumgaertner W.; "Sequence of canine transforming growth factor beta 1 mRNA
                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID CONFLICT
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                                                                                                                          Submitted (FEB-2001) to the EMBL/GenBank/DDBJ
                                                                                                                                          cells."
                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                     Canis familiaris (Dog).
                                                                                                                                                                                                                                                 Transforming growth factor beta 1 (Fragment).
                                                                                                                                                                                                  NCBI_TaxID=9615;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nterPro; IPR001839; TGFb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: TGF-BETA 1 IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROLS PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELLS TYPES. MANY CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF THEM HAVE SPECIFIC RECEPTORS FOR THE PEPTIDE. TGF-BETA 1 REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS. SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                            LPIVYYVGRKPKVEQLSNMIVRSYKCS
                                                                                                                                                                                                                                                                                                                                                                                                                      KDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAGPCCVPQALEP 103
                                                                                                                                                                                                                                                                                                                                                                                                                                      KDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEP 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MATPLERAQHLQSSRHRR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           x60296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PD000357; TGFb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PS00250;
   124 AA;
                124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130 AA;
                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25
25
25
95
95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Y: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY CAB42838.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mitogen; Glycoprotein.
                                                              TGFb;
               124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGF_BETA_1; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18
130
34
96
129
95
93
  14329 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14997 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 691.5; DB 1
Pred. No. 2.4e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERCHAIN (BY SIMILARITY).
G -> S (IN REF. 2).
: 8B41DD6CF39CCA77 CRC64;
                                                 UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSFORMING
                                                                                                                                                                                                                                                                                                               PRT;
21D185218E5556DB CRC64;
                                                                                                            TGF-BETA FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                            130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----ALDTNYCFSSTEKNCCVRQLYIDFR 43
                                                                                                                                                                                                                                                                                                               124 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GROWTH FACTOR BETA 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 11;
                                                                                                                        databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 130;
                                                                                                                                                                                                              Euteleostomi;
Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17;
                                                                                                                                                 in DH82-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CELL
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Q98854
ID Q9885
AC Q9
                                                                                                                                                                                                                        Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                            NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide;
ProDom; PD000357; TGFb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Isolation of transforming growth factor-beta2 cDNA from Cyprinus carpio by RT-PCR.";
Gene 191:103-107(1997).
-!- FUNCTION: TGF-BETA 2 HAS SUPPRESSIVE EFFECTS ON INTER-
DEPENDENT T-CELL GROWTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Actinopterygii; Neopterygii; Teleostel; Ostariophysi; Cypriniformes; Ocyprinidae; Cyprinidae; Cyprinid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1997 (TrEMBLrel. 02,
01-FEB-1997 (TrEMBLrel. 02,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U66874; AAB62983.1; HSSP; P08112; 2TGI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cyprinus carpio (Common carp).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Transforming growth factor beta 2 (TGF-beta 2) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q98854;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q98854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY)
-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-97354301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=7962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        264 PLERAQHLHSSRHRRALDTNSYPYDVPDYASLALDTNYCFSSTEKNCCVRQLYIDFRKDL 323
                                                                                                                        52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44
                                              1 QILCKLKLSCPP---EIYPEPEEVSRDIIAIYNSTRDLLQEKANERAATCERQRTGEEYY 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VYYVGRKPKVEQLSNMIVRSC 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPI
                                                                                                          QILSKLRLASPPSQGDVPPGP--LPEAVLALYNSTRDRVAGESVEPEPEPE-----ADYY 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VYYVGRKPKVEQLSNMIVRSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPI 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLERAQHLHSSRQRR--------ALDTNYCFSSTEKNCCVRQLYIDFRKDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SM00204; TGFB; 1.
E; PS00250; TGF_BETA_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      factor;
                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                            AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mitogen; Glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=9210595;
                                                                                                                                                                                                                                                                                                                                                     257
361
273
335
334
30
199
199
                                                                                                                                                                                                                                                                                                                        41931 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31.2%;
87.2%;
                                                                                                                                                                                                              31.28;
                                                                                                                                                                                     54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                              Score 673.5; DB 13;
Pred. No. 3.7e-50;
4; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                          INTERCHAIN (BY SIMILARITY).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 674.5; DB 6; Pred. No. 6.6e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSFORMING GROWTH FACTOR BETA
                                                                                                                                                                                                                                                                                                                     94D930FA970A3FD3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ON INTERLEUKIN-2
                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                 Length 361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a fish,
                                                                                                                                                                              59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17;
                                                                                                                                                                              Gaps
                                                                                                                                                                              14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        بر
          AID DO COCCOCCERRAR RANK ROCCOCCE DO COCCE DO CO
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                                                                       DISULFID
DISULFID
DISULFID
DISULFID
       DISULFID CONFLICT
                                                                                                                                                                                                              NON_TER
                                                                                                                                                                                                                                          PROSITE; PSUUZJU,
PROMITH factor; Mitogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inoue K., Kawabe Y., Kodama T.;

Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: TGF-BETA 1 IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROLS

-!- FUNCTION: TGF-BETA 1 IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROLS

--- PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL

TYPES. MANY CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF

THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1

REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND

DETERMINES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.

-!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                              ProDom; PD000357; TGFb; 1.
SMART; SM00204; TGFB; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002400; GF_cysknot.
InterPro; IPR001839; TGFb.
Pfam; PF00019; TGF-beta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Transforming growth factor beta 1 (TGF-beta 1) (Fragment).
TGFB1 OR TGF-BETA-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Taylor T.K., James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00438; GFCYSKNOT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Taylor T.K., James E.R., McGonigle S., Yoho E.R., Submitted (APR-1997) to the EMBL/GenBank/DDBJ dat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryctolagus cuniculus (Rabbit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P01137; 1KLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 2-99 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        002730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        002730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AKEVTRVLM---VESGNQIYDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QDLEPLTILYYIGKTPKIEQLSNM 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YIDFKKDLGWKWIHEPKGYNANFCAGACPYLWSADTQHSNILGLYNTINPEASASPCCVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHLLLMLLPSYRLESQHKS-HRQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NPKARVSEQRIELYQILGHKDLTSPTQRYIDSKVVRTRTEGEWLSFDVTEAVSEWLLHRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFLLLMATPLERAQHLHSSRHRRALDTNSYPYDVPDYASLALDTNYCFSSTEKNCCVRQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AKEVHKIDMQPFYPAENVIPTKHY-NPYFRRLRFDVSSMEKNASN---LVKAELRIFRLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF000133; AAB53806.1; AB020217; BAA36950.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     097501;
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                                                                                                                                                                                                                                                                              Glycoprotein.
TRANSFORMING GROWTH FACTOR BETA 1.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIAN (BY SIMILARITY).
LD -> FS (IN REF. 2).
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В 80

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RESULT 15
Q9TV08
ID Q9TV0
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Q921T1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity Matches 119; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
[-- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
EMBL; BC011055; AAH11055.1; -.
MGD; MGI:98726; Tgfb2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb_N.
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1.
ProDom; PD000357; TGFb; 1.
PROSITE; PS00250; TGF_BETA_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090; `
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
similar to transforming growth factor, beta 2.
 80AL60
                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycoprotein.
SEQUENCE 255 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q921T1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               296 ALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSK 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      356 VLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 407
                                                                            227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EQUENCE FROM N.A.
                                                                                                                                                                  319
                                                                                                                                                                                                                                                                                      219
                                                                                                                                                                                                                                                                                                                                              163 KVEQ--HVELYQK--YSNDSWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFR 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 VLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS
                                                                                                                                                                                                                                                          63
                                                                                                                                                                                              LLMLLPSYRLESQQSSRRKKR-------ALDAAYCFRNVQDNCCLRPLYID 166
                                                                                                                                                                                                                                                                                    LSAHSSS------DSKDNTLHVE---INGFNSGRRGDLATIHGMNR-----PFL 258
                                                                                                                                                                                                                                                                                                                  RVEEATHVQILKSKDLTSPTQRYIDSKVVKTRAEGEWLSFDVTDAVQEWLHHKDRNLGFK 62
                                                                            EPLTILYYIGNTPKIEQLSNMIVKSCKCS
                                                                                                       EPLPIVYYVGRKPKVEQLSNMIVRSCKCS 407
                                                                                                                                    FKRDLGWKWIHEPKGYNANFCAGACPYLWSSDTQHTKVLSLYNTINPEASASPCCVSQDL
                                                                                                                                                  FRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQAL 378
                                                                                                                                                                                                                            LLMATPLERAQHLHSSRHRRALDTNSYPYDVPDYASLALDTNYCFSSTEKNCCVRQLYID 318
                                                                                                                                                                                                                                                          ISLHCPCCTFVPSNNYIIPNKSEELEARFAGIDGTSTYASGDQKTIKSTRKKTSGKTPHL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85
112 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29.6%; Score 638; DB 6; ilarity 100.0%; Pred. No. 8.4e-48; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                       29087 MW; 94540017F3C5C219 CRC64;
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12795 MW;
                                                                                                                                                                                                                                                                                                                                                                                          27.8%;
                                                                                                                                                                                                                                                                                                                                                                            42; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                  Score 600; DB 11,
No. 5.4e-44;
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 PRT;
                                                                            255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                255
   127
                                                                                                                                                                                                                                                                                                                                                                                                         DB 11;
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                                                                                                                                                                                                                                                                                                                                                                                                        Length 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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Search completed: April 15, Job time : 83 secs
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Best Local Similarity
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Transforming growth factor beta-1 (Fragment).
Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

German A.J., Helps C.R., Hall E.J., Day M.J.;

"Cloning and sequencing of canine transforming growth factor beta mRNA.";
                                                                                                                                                                                                                                                                                                              NON_TER
                                                                                                                                                                                                                                                                                                                                                                     Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases. EMBL; AF091135; AAD46993.1; -. HSSP; P01137; IXLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                           InterPro; IPR0011111; TGFb_N.
Pfam; PF00688; TGFb_propeptide;
                                                           104
                                                                                                                                                   239
                                                                                                                                                                                               179 WRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEING 238
                                                                                                                       61
                                                                                                                                                                               1 WRYLSNRLLAPSDTPEWLSFDVTGVVRQWLSHGGEVEGFRLSAHCSCDSKDNTLQVDING
                                                          TNYCFSSTEKNCCVRQLYFDFRKD
                                                                                                                                     FNSGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNSYPYDVPDYASLALD 298
                                                                                       TNYCFSSTEKNCCVRQLYIDFRKD 322
                                                                                                                       FSSSRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRQRR---
                                                                                                                                                                                                                                                                                                127 1
127 AA;
                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                127
14641 MW; D46D24ECA89F58DE CRC64;
                                                                                                                                                                                                                                        27.1%; Score 584.5; DB 6; 77.8%; Pred. No. 4.4e-43; tive 5; Mismatches 10;
               2003, 12:00:28
                                                             127
                                                                                                                                                                                                                                                                    Length 127;
                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi;
Canis.
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                                                                                                                        -ALD
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Title:
Perfect score:
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No.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                   Database :
  pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
 2030.5
1916.5
1914.5
11914.5
11839.5
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11826.5
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2159
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  SwissProt_40:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                               Length DB
  TGF1_PIG
TGF1_HUMAN
TGF1_CANFA
TGF1_CANFA
TGF1_RAT
TGF1_CAVPO
TGF1_CAVPO
TGF1_CAVPO
TGF1_CAVPO
TGF1_CHICK
TGF1_SHAM
TGF3_PIG
TGF3_HOMSE
TGF3_HOMSE
TGF3_HOMSE
TGF3_HOMSE
TGF3_HOMSE
TGF3_HOMSE
TGF3_HOMSE
TGF3_HOMSE
TGF2_HUMAN
TGF2_KOMSE
TGF2_HOMAN
TGF2_PIG
TGF2_BOVIN
TGF2_BOVIN
TGF2_BOVIN
TGF2_BOPB_PIG
GDF8_HUMAN
TGF2_BOPB
GDF8_HUMAN
TGF2_BOPB
GDF8_HUMAN
TGF2_BOPB
GDF8_HUMAN
TGF2_BOPB
GDF8_HUMAN
TGF8_BOPB
GDF8_HUMAN
TGF8_BOPB
GDF8_HUMAN
TGF8_BOPB
GDF8_HUMAN
TGF8_BOPB
GDF8_HUMAN
TGF8_BOUSE
                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                          P17246 rattus norv
Q9z1y6 cavia porce
P18341 bos taurus
P09531 gallus gall
P16176 xenopus lae
P16047 gallus gall
                                                                                                                 p09531 gallus gall
p16176 xenopus lae
p16047 gallus gall
p15203 sus scrofa
p17125 mus musculu
Q07258 rattus norv
p10600 homo sapien
p27090 mus musculu
p08112 homo sapien
p17247 xenopus lae
p30371 gallus gall
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019011 equus cabal
P04202 mus musculu
P17246 rattus norv
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P011137 homo sapie
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4 bos taurus
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                                homo sapien
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16:8730- SEQUENCE: SEQUENCE: //ations (1/2) PubMed=2/2	ode 33	7, La: 1, La: fact: Chor Ceta Ceta ubMed ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;	DARD;	407 375 374 425 424 424 426 426
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Pfam: PF000188; TGFb_propeptide; 1
PRINTS; PR00438; GFCYSKNOT.
PRINTS; PR01423; TGFBETA.
ProDom: PD000357; TGFb; 1.
SMART; SM00204; TGFB; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
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PIR; A27512; A27512.
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InterPro; IPR003911; TGF_TGFb.
InterPro; IPR001839; TGFb.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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               SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNSYPYDVPDYASLALDTN
                                                      YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHCSCDSKDNTLHVEINGFN
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CAUTION: REF.3 SEQUENCE WHICH WAS SAID TO ORIGINATE FROM CHICKEN
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R -> G (IN REF. 3).
N -> NA (IN REF. 3).
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Pfam; PF00688; TGFb_propeptide;
PRINTS; PR00438; GFCYSKNOT.
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"Growth factor expression in skin during wool follicle development.";

Comp. Biochem. Physiol. 110B:697-705(1995).

-I- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL

PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL

TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM

HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE

ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES

A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.

I SUBUNIT: HOMODIMER; DISULFIDE-LINKED.

SUBCELLULAR LOCATION: Secreted.
                                                                                                                  PROSITE; PS00250;
                                                                                                                                                                                                                                                                                         InterPro; IPR002400; GF_cysknot.
InterPro; IPR003911; TGF_TGFb.
InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb_N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE~95121932; PubMed~7821809;
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Bovidae; Caprinae; Ovis.
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        h factor; Mitogen; G
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                                                                                          ; PD000000; SM00204; TGFB; 1. SM00204; TGF_BETA_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 license agreement (See http://www.isb-sib.ch/announce/
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                                                            Glycoprotein; Signal.
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POTENTIAL.
TRANSFORMING GROWTH FACTOR BETA 1.
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TGF1_HUMAN STANDARD,
P01137; Q9UCG4;
21-UUL-1986 (Rel. 01, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2007 (Rel. 41, Last annotation update)
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SITE
                    SEQUENCE FROM N.A.

MEDLINE-85296301; PubMed-3861940;

MEDLINE-85296301; PubMed-3861940;

Derynck R., Jarrett J.A., Chen E.Y., Eaton D.H., Bell J.R.,

Derynck R.K., Roberts A.B., Sporn M.B., Goeddel D.V.;

"Human transforming growth factor-beta complementary DNA se
expression in normal and transformed cells.";

Nature 316:701-705(1985).
                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE-87174845; PubMed-3470709;

Derynck R., Rhee L., Chen E.Y., van Ti
"Intron-exon structure of the human tr
precursor gene.";

Nucleic Acids Res. 15:3188-3189(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; P
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Primates;
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89.7%;
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
MW; 1C247299484D0E57 CRC64;
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                                                                                                                                                                                                                                                                         growth factor-beta
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Tumor [5]
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                                                                                                                                                                          Growth factor beta 2.";

Biochemistry 35:8517-8534(1996).

IF PUNCTION: MULTIFUNCTIONAL PERTIDE THAT CONTROLS PROLIFERATION, DIFFERNTIATION, AND OTHER FUNCTIONS IN MANY CELL TYPES. MANY CELL TYPES. MANY CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTALLY ALL OF THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1 REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.

ISUBCULIULAR LOCATION: Secreted.

SUBCELLULAR LOCATION: Secreted.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRUCTURE BY NMR OF 279-390.
MEDLINE=96266150; PubMed=8679613;
Hinck A.P., Archer S.J., Qian S.W.,
Weatherbee J.A., Tsang M.L.-S., Luca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Transforming growth factor beta 1: NMR signal assignments of recombinant protein expressed and isotopically enriched using hamster ovary cells.";
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MEDLINE-93144319; PubMed-8424942;
Archer S.J., Bax A., Roberts A.B., Spo
Weatherbee J.A., Tsang M.L.-S., Lucas
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Massague J., Like B.;
"Cellular receptors for type beta transforming growth factor. L
binding and affinity labeling in human and rodent cell lines.";
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Bourdrel L., Lin C.-H., Lauren S.L., Elmore R.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Bladder carcinoma;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Transforming growth factor beta solution and comparison with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           by heteronuclear magnetic resonance Biochemistry 32:1164-1171(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Archer S.J., Bax A., Roberts A.B., Sporn M. Weatherbee J.A., Tsang M.L.-S., Lucas R., 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochemistry 32:1152-1163(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Torchia D.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Forchia D.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lucas
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1: three-dimensional structure X-ray structure of transforming
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Roberts A.B., Sporn
as R., Zheng B.-L., V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   spectroscopy.";
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Zheng B.-L.,
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.., Wenker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               м.в.,
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J.,
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J.,
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Best Local S
Matches 365
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InterPro; IPR001111; TGFb.N.
Pfam; PF000019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1.
PRINTS; PR00438; GFCYSKNOT.
PRINTS; PR01423; TGFBETA.
PRODOM; PD000357; TGFB; 1.
SMART; SM00204; TGFB; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR: A22290. A22290.

PIR: A27513. A27513.

PDB: 1KLA: 17-AUG-96.

PDB: 1KLC: 17-AUG-96.

PDB: 1KLD: 17-AUG-96.

PDB: 1KLD: 17-AUG-96.

Genew: HGNC: 11766; TGFB1.

MIM: 190180:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS0025
Growth factor;
SIGNAL
                                                                                                                                                                                                                                                                                                                    CARBOHYD
SITE
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                    DISULFID
DISULFID
DISULFID
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002400; GF_cysknot.
InterPro; IPR003911; TGF_TGFb.
InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb_N.
                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                  181
                         241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L; X05839; CAA29283.1; JOINED.
L; X05844; CAA29283.1; JOINED.
L; X05844; CAA29283.1; JOINED.
L; X05849; CAA29283.1; JOINED.
L; X05849; CAA29283.1; JOINED.
L; X05850; CAA29283.1; JOINED.
L; X05850; CAA29283.1; JOINED.
L; X02812; CAA26580.1; ALT_SEQ.
L; BC001180; AAH01180.1; -...
L; BC00125; AAH0125.1; -...
L; BC022242; AAH22242.1; -...
L; M38449; AAA36735.1; -...
L; M38449; AAA36735.1; -...
                                                             YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN
TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR---
                                                                                                                                                                                                                  MAPSGLRLLPLLMLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA
                                                                                                              YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
                                                                                                                                                                SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
                       SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDINSYPYDVPDYASLALDIN
                                               YLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFT
                                                                                                                                                   SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
                                                                                                                                                                                                    MPPSGLRLLLLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A01395; WFHU2.
                                                                                                  YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLKLKVEQHVELYQKYSNNSWR
                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                       24
279
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                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                        ĀĀ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mitogen;
                                                                                                                                                                                                                                                                                                        44341 MW;
                                                                                                                                                                                                                                                                   88.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein; Signal; 3D-structure
                                                                                                                                                                                                                                                                                                    INTERCHAIN.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

CELL ATTACHMENT SITE (POTENTIAL).

L -> P (IN REF. 2).

R -> RR (IN REF. 2).

R -> R (IN REF. 2).
                                                                                                                                                                                                                                                   Score 1916.5; Db 1,
Pred. No. 4.5e-146;
Pred. No. 15;
                                                                                                                                                                                                                                                       10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSFORMING GROWTH FACTOR BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                              DB 1; Length 390;
                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                       17;
                                                                                                                                                                                                                                                    Gaps
283
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                                                           DISULFID DISULFID
                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                      CHAIN
                                                                                                                                                                                                       InterPro; IPR001111; TGFb_N.
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide;
PRINTS; PR00438; GFCYSKNOT.
PRINTS; PR01423; TGFBETA.
                                DISULFID
                                                                                                                                                                                                                                                                             EMBL; M16658; AAA35369.1; -.
PIR; A26960; A26960;
HSSP; P01137; 1KAA.
Interpro; IPR002400; GF_cysknot.
Interpro; IPR003911; TGF_TGFb.
Interpro; IPR001839; TGFb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cercopithecus aethiops (Green monkey) (Grivet).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Transforming growth factor beta 1 precursor (
                                               DISULFID
                                                                                        DISULFID
                                                                                                                     PROPEP
                                                                                                                                   SIGNAL
                                                                                                                                                  Growth
                                                                                                                                                                PROSITE;
                                                                                                                                                                                SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cloning and sequence analysis of factor-beta cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sharples K., Plowman G.D., Rose T.M., Twardzik D.R., Purchio A.F.; "Cloning and sequence analysis of simian transforming growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=87246074; PubMed=3474130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cercopithecinae; Cercopithecus
NCBI_TaxID=9534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGFB1
                                                                                                                                                                             ProDom; PD000357; TGFb; 1. SMART; SM00204; TGFB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6:239-244(1987).

FUNCTION: MULTIFUNCTIONAL PEPTIDE THAT CONTROL PROLIFERATION DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL TYPES. MAN CELLS SYNTHESIZE TOF-BETA AND ESSENVIALLY ALL OF THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
SUBCELLULAR LOCATION: Secreted.
SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY
                                                                                                                                                  factor;
                                                                                                                                                                PS00250;
    279
285
293
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326
355
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136
                                                                                                                                  Mitogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                TGF_BETA_1; 1.
                                                                                                                                               Glycoprotein;
TRANSFORMING GROWTH FACTOR BI
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTEN
                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               precursor (TGF-beta
                                                                                                                                               Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vertebrata; Euteleostomi;
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                                                                                                      FACTOR BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROLIFERATION.
   (POTENTIAL).
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RESULT 5
TGF1_CANFA
ID TGF1_C
AC P54831
DT 01-CCT
DT 01-CCT
DT 01-CCT
DT 01-CCT
CC Mammal
RC TISSUE
RC MEDLIN
RA MED
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                                                                                                                                                                                       RC TISSUE-Jugular vein endothelial;

R MEDLINE-95237630; PubMed-7721110;

RA Manning A.M., Auchampach J.A., Drong R.F., Slightom J.L.;

RA Manning A.M., Auchampach J.A., Drong R.F., Slightom J.L.;

RA Manning A.M., Auchampach J.A., Drong R.F., Slightom J.L.;

RA Manning A.M., Auchampach J.A., Drong R.F., Slightom J.L.;

RT factor-beta 1-encoding gene.";

RI Gene 155:307-308(1995).

C1- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL

C2- PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELLS

C3- TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM

C4- TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND DETERMINES

C5- ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES

C6- ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES

C7- SUBGULTUAR LOCATION: Secreted.

C7- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
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between
     use by
modified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; (Mammalia; Eutheria; Carnivora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGF1_CANFA P54831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transforming growth factor beta 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       344
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                                                s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAPSGLRLLPLLWLLWLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA
                                                                                                                                                                SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN
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     institutions as long atement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1914.5;
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                      There are no restrictions on ong as its content is in no
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PRINTS; PR01423; TGFBETA.
ProDom; PD000357; TGFb; 1.
SMART; SM00204; TGFB; 1.
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InterPro; IPR003911; TGF_TGFb.
InterPro; IPR00133; TGFb_N.
InterPro; IPR001111; TGFb_N.
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HSSP; P01137; 1KLA.
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2; Mismatches 17;
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N-LINKED (GLCNAC. . .)
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019011; 15-JUL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation updat Transforming growth factor beta 1 precursor

annotation update) beta 1 precursor (

(TGF-beta 1).

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Pran; process; Terbeta; 1
PRINTS; process; Grecysknot;
PRINTS; pro1423; Terbeta; 1
Probom; pro0357; Terb; 1
SMART; SM00204; Terb; 1
PROSITE; PS00250; Terbeta; 1
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Cloning and sequencing of equine transforming growth factor-beta 1
(TGF beta-1) cDNA.";
DNA seq. 7:375-378(1997).

PROCIFERATION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002400; GF_cysknot.
InterPro; IPR003911; TGF_TGFb.
InterPro; IPR001839; TGFb.
InterPro; IPR001111; TGFb_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X99438; CAA67801.1; -. HSSP; P01137; 1KLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Penha-Goncalves M.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98185507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBI_TaxID=9796;
       121
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                                                                              121
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SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A POSITIVE OR NEGATIVE DIRECTION OF T SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
                                                                                                                                                                                                                                                                                             YKTVETGSHSIYMFFNTSELRAAVPDPMLLSRAELRLLRLKLSVEQHVELYQKYSNNSWR
                                                                  YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
                                                                                                                                                                                    SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
                                                                                                                                                                                                                                                                                                                                                                        MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
                                                                                                                                                SPPSQGEVPPGPLPEAVLALYNSTRAQVAGESAETEPEPEADYYAKEVTRVLMVEKENEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ĀĀ,
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86.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Onions D.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein; Signal.
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OCICHAC. . .) (POTEN CONTENT C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1839.5;
Pred. No. 6.66
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TRANSFORMING GROWTH FACTOR BETA
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BY SIMILAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6e-140;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
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                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                     Poirot L., Benoist C., Mathis D.;

"Transforming growth factor-beta 1 sequence and expression: no difference between NOD/Lt and C57B1/6 mouse strains.";

Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENITALY ALL OF THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.

-!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.

-!- SUBCELLULAR LOCATION: Secreted.
                            EMBL;
                                                                                                                                           modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Molecular organization of the gene encoding murine transforming growth factor beta 1.";
Gene 166.376.376.376.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Derynck R., Jarrett J.A., Chen E.Y., Goeddel "The murine transforming growth factor-beta J. Biol. Chem. 261:4377-4379(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE-86168129; PubMed-3007454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUN-2002 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene 165:325-326(1995).
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15-JUN-2002
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; M13177; AAA40423.1;
; L42462; AAB00138.1;
; L42456; AAB00138.1;
; L42457; AAB00138.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NQHNPGASAAPCCVPQVLEPLPIVYYVGRKPKVEQLSNMIVRSCKCS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and NOD/LT; TISSUE=Spleen;
ist C., Mathis D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Goeddel D.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  390 AA.
                                                                                                                                                                                                                              There are no restrictions ong as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         precursor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALDIN
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RESULT 8
TGF1_RAT
ID TGF1
AC P172
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DT 01-2
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Best Local :
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    TGF1_RAT
P17246;
01-AUG-1990
01-AUG-1990
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CARBOHYD
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pfam; pr00688; TGFb_propeptide;
pRINTS; pr00438; GFCYSKNOT.
pRINTS; pr01423; TGFBETA.
ProDom; pD000357; TGFb; 1.
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InterPro; IPR003911; TGF_TGFb.
InterPro; IPR001839; TGFb.
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EMBL; L42459; AAB00138.1; J0
EMBL; L42460; AAB00138.1; J0
EMBL; L42461; AAB00138.1; J0
EMBL; L42461; AAB00138.1; J0
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                                                                                                                                                           NQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 407
                                                                                                                                                                                                                                      PKRRGDLGTIHDMNRPFLLLMATPLERAQHLHSSRHRR-------ALDTN
                                                                                                                                                                                                                                                                                                                                        SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNSYPYDVPDYASLALDTN
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PS00250; TGF_BETA_1; 1.
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390
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(Rel. 15, Created)
(Rel. 15, Last sequence update)
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1 23
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                                                              STANDARD;
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85.0%;
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                                                                390
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Query Match
Best Local
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InterPro; IPR003911; TGF_TGFb.
InterPro; IPR001839; TGFb.
InterPro; IPR0011111; TGFb.N.
Pfam; PF00019; TGF-beta; I.
Pfam; PF00019; TGF-beta; I.
Pfam; PF00688; TGFb_propeptide; 1.
PRINTS; PR00438; GFCYSKNOT.
PRINTS; PR01423; TGFBETA.
ProDom; PD000357; TGFB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qian S.W., Kondaiah P., Roberts A.B., Sporn M.B.;

Qian S.W., Kondaiah P., Roberts A.B., Sporn M.B.;

"CDNA cloning by PCR of rat transforming growth factor beta-1.";

Nucleic Acids Res. 18:3059-3059(1990).

-i- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL TYPES. MANY CELLS SYMTHESIZE TGF-BETA AND ESSENTIALY ALL OF THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.

-i- SUBGULT: HOMODIMER; DISULFIDE-LINKED.
                                                                                                                                                                                              SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                             DISULFID DISULFID
                                                                                                                                                                                                                                                                                                                  DISULFID DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as Its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Sprague-Dawley; TISSUE=Hea MEDLINE=90272425; PubMed=2349108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUN-2002 (Rel. 41, Last annotation update)
Transforming growth factor beta 1 precursor (TGF-beta 1).
                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S10219, S10219.
X52498; CAA36741.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SM00204; TGFB; 1.
E: PS00250; TGF_BETA_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   factor;
                                                                                                                  Similarity
                                                                                                                                                                                              390
                                                                                             Conservative
                                                                                                                                                                                                                                         Mitogen;
1 1 23
24 2 23
25 390
390
393 356
355 389
266 389
355 389
355 389
356 136
                                                                                                                                                                                              AA;
                                                                                                                                                                                              44329
                                                                                                                       85.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Heart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycoprotein; Signal.
                                                                                                                                                                                              MW,
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                                                                                                                                                                                      BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

OF SIMILARITY.
                                                                                        Pred. No. 1.46
4; Mismatches
                                                                                                                       Score 1835.5;
Pred. No. 1.4e
                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSFORMING GROWTH FACTOR BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                       .4e-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    n M.B.;
--wth factor /
                                                                                                                       DB 1;
e-139;
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                                                                                                Indels
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                                                                                                Gaps
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RESULT 9
TGF1 CAVPO
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TGF1_CAVPO STANDARD;
Q9Z1Y6; Q9QZB3; Q9R148;
16-CCT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Transforming growth factor beta 1 precursor (
the European Bioinformatics Institute. Ther use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See For send an email to license@isb-sib.ch).
                                                                                               between
the Euro
                                                                                                                                                                                                                                            "Gilinea-pig transforming growth factor-beta expression in injured tracheal epithelium.";

tracheal epithelium.";

Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: MULTIFUNCTIONAL PEPTIDE THAT CONTROLS PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL TYPES. MANY CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF THEM HAVE SPECITIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1 REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.

POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-Hartley; TISS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tissues."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99144670; PubMed=10025978;
Scarozza A.M., Ramsingh A.I., Wicher V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Guinea pig transforming after BCG vaccination.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sekizawa K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 279-371 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Spontaneous cytokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 265-382 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jeevan A., McMurray D.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-Hartley;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10141;
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                                                                                                                                                                                  SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                             SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY). SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR
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chida Y., Nomura
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growth factor-beta in
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Hystricognathi; Caviidae;
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                          (See http://www.isb-sib.ch/announce/
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                                                                There are no restrictions ong as its content is in
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normal guinea pig blood
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RESULT 10
TGF1_BOVIN
ID TGF1_B
AC P18341
DT 01-NOV
DT 01-NOV

STANDARD;

315 AA

TGF1_BOVIN P18341; 01-NOV-1990 01-NOV-1990

(Rel. 16, Created)
(Rel. 16, Last sequence

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Pfam; PF00688; TGFb_propeptide;
PRINTS; PR01423; TGFBETA.
ProDom; PR000357; TGFb; 1.
SMART; SM00204; TGFB; 1.
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SIGNAL
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EMBL; AF097509; AAC83807.1;
EMBL; AF169347; AAD49347.1;
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InterPro; IPR001111; TGFb_N.
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344
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                                                                                                             PKRRGDLAAIHGMNRPFLLLMATPLERAQHLHSSRHRR-------
             NQHNPGASAAPCCVPQALEPLPIVYYYGRKPKVEQLSNMIVRSCKCS 407
                                                   YCFSSTEKNCCYRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY YCFSSTEKNCCYRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY
                                                                                                                                                                                    YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN
                                                                                                                                                                                                                                             YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR
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                                                                                                                                                                                                                                                                                                                                              MPPSRLRLLPLLLPLLWLLVLAPGRPASGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA
NQHNPGASAAPCCVPQALEPLPIVYYVGRKAKVEQLSNMIVRSCKCS
                                                                                                                                          SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNSYPYDVPDYASLALDTN
                                                                                                                                                                     YLSNQLLTPSDTPEWLSFDVTGVVRQWLSQGEELEGFRFSAHCSCDSKDNTLRVEINGIG
                                                                                                                                                                                                                                                                                      SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEPDYYAKEVTRVLMVDNSHNI
                                                                                                                                                                                                                             YKSIETVAHSIYMFFNTSELREAVPDPLLLSRAELRMQRLKLNVEQHVELYQKYSNNSWR
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N-LINKED (GLONAC. . ) (
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CELL ATTACHMENT SITE (PO
G -> P (IN REF. 2) .
K -> S (IN REF. 2) .
K -> G (IN REF. 2) .
A -> G (IN REF. 2) .
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AC. . .) (POTENTIAL).
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Matches
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J. Biol. Chem. 267:2325-2328(1992).
-i. FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENITALLY ALL OF THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
                                                                                                                                                              DISULFID DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-92129307; PubMed-1733936; Ogawa Y., Schmidt D.K., Dasch J.R., Chang R.J., Glaser C.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      growth factor-beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Bone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complementary deoxyribonucleic acid cloning of bovine transforming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 van Obberghen-Schilling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-91042552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUN-2002 (Rel. 41, Last annotation update)
Transforming growth factor beta 1 precursor (TGF-beta 1) (Fragment).
                                                                                                                                                                                                                                                                                                  Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1.
ProDom; PD000357; TGFb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                          Growth
                                                                                                                                                                                                                                                                                        SMART;
                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001839; TGFb.
InterPro; IPR0011111; TGFb_N.
                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M36271; AAA30778.1; -.
                                                          SEQUENCE
                                                                                     CARBOHYD
                                                                                                                   CARBOHYD
                                                                                                                                   DISULFID
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                                                                                                                                                                                              DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HAVE BEEN FOUND IN BONE.
SUBCELLULAR LOCATION: Secreted.
SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: HOMODIMER; DISULFIDE-LINKED. HETERODIMERS OF TGF-BETA 1/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
                                                                                                                                                                                                                                                                                                                                                                             A40057; A40057.
; P01137; 1KLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Endocrinol. 1:693-698(1987).
 295;
                                                                                                                                                                                                                                                                       SM00204; TGFB; 1.
E; PS00250; TGF_BETA_1; 1.
                                                                                                                                                                                                                                                          factor;
              Similarity
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210
218
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 Conservative
                                                                                                                                                                                                                                                       Mitogen;
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              72.8%;
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                                                                                                                                                                                                                                                       Glycoprotein.
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                                                                    TRANSFORMING GROWTH FACTOR BETA 1.
BY SIMILARITY.
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INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
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 9
            Score 1572.5;
Pred. No. 1.2
                                                          C2717A23D994E00E CRC64;
 Mismatches
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               .2e-118;
                              DB 1;
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Gaps
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76 AVLALYNSTRDRVAGESVEPEPEADYYAKEVTRVLMVESGNQIYDKFKGTPHSLYMLF 135

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RESULT 11
TGF1_CHICK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-White leghorn;
MEDLINE-89112198; PubMed=2464131;
Jakowlew S.B., Dillard P.J., Sporn M.B., Roberts A.B.;
"Complementary deoxyribonucleic acid cloning of a messenge ribonucleic acid encoding transforming growth factor beta chicken embryo chondrocytes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Transforming growth factor beta 1 precursor (TGF-beta 1) (TGF-beta 4)
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                                                                                                                                                                                                                                                                 factor-beta 4 complementary DNA.";

Mol. Endocrinol. 6:989-992(1992).

-i- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL

-i- FUNCTION. DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL

TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM

HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mol.
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                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=92357039; PubMed=1353860;
Burt D.W., Jakowlew S.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Fragment).
                                                                                                                                                                        -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                      "Correction: a new interpretation of a chicken transforming growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        224 YIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               316
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                                                                                                                                                                                                            ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS. SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
                                                                                                                                                                                            SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFLLLMATPLERAQHLHSSRHRRALDTNSYPYDVPDYASLALDTNYCFSSTEKNCCVRQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFNSGRRGDLATIHGMNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NTSELREAVPEPVLLSRADVRLLRLKLKVEQHVELYQKYSNNSWRYLSNRLLAPSDSPEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NTSELREAVPEPVILSRAELRILRIKIKVEQHVEIYQKYSNDSWRYISNRILAPSDSPEW 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFLLLMATPLERAQHLHSSRHRR---------ALDTNYCFSSTEKNCCVRQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LSFDVTGVVRQWLTRREEIEGFRLSAHCSCDSKDNTLQVDINGFSSGRRGDLATIHGMNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Endocrinol. 2:1186-1195(1988).
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M31160;

AAB05637.1;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPRO01839; TGFb.
InterPro; IPRO01111; TGFb_N.
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGFb_propeptide; 1
ProDom; PD000357; TGFb; 1.
SMART; SM00204; TGFB; 1.
P16176;

01-APR-1990 (Rel. 14, Created)

01-APR-1990 (Rel. 14, Last sequence update)

15-JUN-2002 (Rel. 41, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

Transforming growth factor beta 1 precursor (TGF-beta 1) (TGF-beta 2)

Xenopus laevis (African clawed frog).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibla; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

Xenopodinae; Xenopus.
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DISULFID
DISULFID
DISULFID
DISULFID
CARBOHYD
CARBOHYD
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                                                                                                                                             XENLA
                                                                                                                                 TGF1_XENLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVPPGPLPEAVLALYNSTRDRVA 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A34941; A34941.
S03110; S03110.
                                                                                                                                                                                            TLDPLPIIYYVGRNVRVEQLSNMVVRACKCS
                                                                                                                                                                                                                                           IDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQ 376
                                                                                                                                                                                                                                                                                                                       LLMATPLERAQHLHSSRHRRALDTNSYPYDVPDYASLALDTNYCF--SSTEKNCCVRQLY
                                                                                                                                                                                                                                                                                                                                                 VHQWLSGSELLGVFKLSVHCPCEMGPGHAEEMRISIEGFEQ-QRGDMQSIAKKHRRVPYV
                                                                                                                                                                                                                                                                                                                                                                         VRQWLTRREAIEGFRLSAHSSSD---SKDNTLHVEINGFNSGRRGDLATIHGMNR--PFL 258
                                                                                                                                                                                                           ALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 407
                                                                                                                                                                                                                                                                                                  LAMALPAERANELHSARRRR---
                                                                                                                                                                                                                                                                                                                                                                                                  LLHRAELRMLRQKAAADSAGTEQRLELYQGYGNASWRYLHGRSVRATADDEWLSFDVTDA 180
                                                                                                                                                                                                                                                                                                                                                                                                                            LLSRAELRLLRLKLK-----VEQHVELYQKYSNDSWRYLSNRLLAPSDSPEWLSFDVTGV 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                    QRARLRPPPDGPDEYWAKELRRIPMETTWDGAMEHWQPQSHSIFFVFNVSRARRG-GRPT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GES-VEPEPEPEADYYAKEVTRVLMVESGNQIYDKFKGTPHSLYMLFNTSELREAVPEPV 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSTCQRLDLEAAKKKRIEAVRGQILSKLRLTAPPPASETPPRPLPDDVRALYNSTQELLK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P01137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mitogen; Glycoprotein; Signal.
                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   259
373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48.5%; Score 1047; DB 1; 52.9%; Pred. No. 1.8e-76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
BY SIMILARITY.
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N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

CELL ATTACHMENT SITE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
TRANSFORMING GROWTH FACTOR BETA 1.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9903F3479C8552E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY.
SIMILARITY.
                                                                                                                                                                                              373
                                                                                                                               382 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 373;
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Best Local
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Pfam; Pr00019; TGF-beta; 1.
Pfam; Pr00688; TGFb_propeptide; 1
Pfam; Pr00688; GFCYSKNOT.
PRINTS; PR00438; GFCYSKNOT.
PRINTS; PR01423; TGFBETA.
ProDom; P0000357; TGFB: 1.
SMART; SM00204; TGFB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF009335; AAB64441.1; JOINED. EMBL; AF009331; AAB64441.1; JOINED. EMBL; AF009332; AAB64441.1; JOINED. EMBL; AF009333; AAB64441.1; JOINED. EMBL; AF009334; AAB64441.1; JOINED. PIR; A34929; A34929; A34929; A34929; A34929; A36929; A3692
                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID DISULFID
                                                                                                                                                                                                                                                                                                                                                                                 SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kondaiah P., Sands M.J., Smith J.M., Fields A., Roberts A.B., Sporn M.B., Welton D.A.; Sporn M.B., Welton D.A.; "Identification of a novel transforming growth factor-beta (TGF-beta 5) mRNA in Xenopus laevis."; J. Biol. Chem. 265:1089-1093(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002400;
InterPro; IPR003911;
InterPro; IPR001839;
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
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Submitted (AUG-1997) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00250; TGF_BETA_1;
                             124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=90110090; PubMed=2295601;
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                                                                         60
                                                                                                                     69
FKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKL--KVEQHVELYQKYSNDSW--
                                                                                                                                                                 MEVLWMLLVLLVLHLSSLAMSLSTCKAVDMEEVRKRRIEAIRGQILSKLKLDKTPDV-DS
                                                                                                                                                                                                             LPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDV
                                                                    EKMTVPSEAIFLYNSTLEVIREKATREEEHVGHDQNIQDYYAKQVYR---FESITELED-
                                                                                                                PPGPLPEAVLALYNSTRDRVAGESVEPE-----PEPEADYYAKEVTRVLMVESGNQIYDK 123
                                                                                                                                                                                                                                                                190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J05180; AAA49968.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                factor;
                                                                                                                                                                                                                                                           Similarity 45.9
90; Conservative
                                                                                                                                                                                                                                                                                                                                                           382 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mitogen;
                                                                                                                                                                                                                                                                                      40.2%;
                                                                                                                                                                                                                                                                                                                                                        44200 MW;
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TGF_TGFb.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycoprotein;
                                                                                                                                                                                                                                                                55;
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OF COTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

CELL ATTACHMENT SITE (POTENTIAL).
                                                                                                                                                                                                                                                                               Score 868.5; DB 1
Pred. No. 3.6e-62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSFORMING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                        1034621C917AAE15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GROWTH FACTOR BETA
                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                        CRC64;
                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                       Length 382;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           الالكان gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Eukaryota; Metazoa; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          p16047;
01-APR-1990 (Rel. 14, Createu,
01-APR-1990 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-White leghorn;
MEDLING-95169270; Pubmed-7865129;
Burt D.W., Dey B.R., Paton I.R., Morrice D.R., Law A.S.;
"The chicken transforming growth factor-beta 3 gene: genomic structure, transcriptional analysis, and chromosomal location.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-89096966; PubMed-3211158;
MEDLINE-89096966; PubMed-3211158;
Jakowlew S.B., Dillard P.J., Kondaiah P., Sporn M.B., Roberts A.B.;
Jakowlew S.B., Dillard P.J., Kondaiah P., Sporn M.B., Roberts A.B.;
"Complementary deoxyribonucleic acid cloning of a novel transforming
"Complementary deoxyribonucleic acid from chick embryo
                                                                                                                Jakowlew S.B., Lechleider R., Geiser A.G., Kim S.J., Santa Coloma T.A., Cubert J., Sporn M.B., Roberts A.B., "Identification and characterization of the chicken tragrowth factor-beta 3 promoter."; Mol. Endocrinol. 6:1285-1298(1992).
MOL. Endocrinol. 6:1285-1298(1992).
-i- FUNCTION: INVOLVED IN EMBRYGENESIS AND CELL DIFFER-I-- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
                                                                                                                                                                                                                                                                                                           "Comparative analysis of human and chicken transforming growth factor-beta 2 and -beta 3 promoters.";
J. Mol. Endocrinol. 7:175-183(1991).
                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-White leghorn; TISSUE-Blood; MEDLINE-92134496; PubMed=1840616;
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                                                                                                                                                                                                                                                                                                                                                                         Burt D.W., Dey B.R., Paton I.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-117 FROM N.A.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                    MEDLINE-93024487; PubMed-1406706;
                                                                                                                                                                                                                                                                         SEQUENCE OF 1-117 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell Biol. 14:111-123(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --GVGQEYCFGNNGPNCCVKPLYINFRKDLGWKWIHEPKGYEANYCLGNCPYIWSMDTQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQY
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                                                                           SIMILARITY: BELONGS TO THE TGF-BETA FAMILY
                                                                                                 SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 407
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EMBL; X58127; CAA41128.2; JOINED.
EMBL; X60055; CAA41128.2; JOINED.
EMBL; X60091; CAA41128.2; JOINED.
EMBL; X60090; CAA41128.2; JOINED.
EMBL; X60090; AAB23575.1; -.
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Pfam; PF00019; TGT-beta; 1.
Pfam; PF00688; TGFb_propeptide;
PRINTS; PR01423; TGFBETA.
PRODOM; PD000357; TGFb; 1.
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PROSITE; PS00250; TGF_BETA_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP;
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InterPro; IPR001839; TGFb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YQILALYNSTRELL--EEMEEEKEESCSQENTESEYYAKEIHKFDMIQGLPEHNELGICP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LVLLSLLSFATVSLALSSCTTLDLEHIKKKRVEAIRGQILSKLRLTSPPE--SVGPAHVP
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                                                                                                                                 CLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSN
                                                                                                                                                                                                                                    ALDTNSYPYDVPDYASLALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANF
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MVVKSCKCS
                                                                                                  CSGPCPYLRSADTTHSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSN
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                                                 MIVRSCKCS
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412
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BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
ELPT -> DERQ (IN REF. 1).
ELPT -> DERQ (IN REF. 1).
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Pfam; PF00688; TGFb_propeptide;
PRINTS; PR00438; GFCYSKNOT.
PRINTS; PR01423; TGFBETA.
ProDom; PD000357; TGFb; 1.
SMART; SM00204; TGFB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                       Interpro; IPR002400; GF_cysknot.
Interpro; IPR003911; TGF_TGFb.
Interpro; IPR001839; TGFb.
Interpro; IPR001111; TGFb_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X14150; CAA32363.1; -. PIR; S01825; S01825.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "A new type of transforming growth factor-beta, TGF-beta 3.";
EMBO J. 7:3737-3743(1988).
-i- FUNCTION: INCOLVED IN EMBRYOGENESIS AND CELL DIFFERENTIATION.
-i- SUBGULTI: HOMODIMER; DISULFIDE-LINKED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-89091120; PubMed=3208746; Derynck R., Lindquist B., Lee A., Rhee L., Mason A.J., Miller D.A., Chen E.Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LT 14
PIG
                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                     Growth tactor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-APR-1990 (Rel. 14, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Transforming growth factor beta 3 precursor (TGF-beta 3).
                                                                                                                                                                                                                                                              PROPEP
                                                                                                                                                                                                                                                                                                PROSITE; PS00250; TGF_BETA_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P1.0600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sus scrofa (Pig)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGFB3
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                                15
                                                                     Local
        7
             LLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVPPGPLP 74
LVVLALLNFATVSLSMSTCTTLDFDHIKRKRVEAIRGQILSKLRLTSPPDPSML--ANIP 64
                                                         190;
                                                                    Similarity
                                                                                                             409 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Metazoa;
                                                       Conservative
                                                                                                                                                                                                                                                                     Mitogen; Glycoprotein; Signal
1 18 POTENTIAL.
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313
375
406
408
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374
                                                                                                          46814 MW;
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                                                                38.6%; Score 834; DB 1; 44.6%; Pred. No. 2.3e-59;
                                                         58;
                                                                                                                  INTERCHAIN (BY SIMILARITY).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

CELL ATTACHMENT SITE (POTENTIAL).
                                                                                                                                                                                     TRANSFORMING GROWTH FACTOR BETA
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                          B4900235B5CC955E CRC64;
                                                      Mismatches
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Coffey F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AΑ
                                                                              Length 409;
                                                      Indels
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                                                   Gaps
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RESULT
TGF3_MC
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                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

MEDLINE-91000714; PubMed=2206556;

Denhez F., Lafyatis R., Kondaiah P., Roberts A.B.,

"Cloning by polymerase chain reaction of a new mous
mTGF-beta 3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1990
01-AUG-1990
15-JUN-2002
                             entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                      "Complementary DNA cloning of the murine transforming growth factor-beta 3 (TGF beta 3) precursor and the comparative expression of TGF beta 3 and TGF beta 1 messenger RNA in murine embryos and adult tissues.";

Ol. Endocrinol. 3:1926-1934(1989).
                                                                                                                                                                                     -!- FUNCTION: INVOLVED IN EMBRYOGENESIS AND CELL DIFFERENTIATION
-!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
-!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                  Growth Factors 3:139-146(1990)
                                                                                                                                                                                                                                                                                                                                                            MO1.
                                                                                                                                                                         -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FKUM N.A.
MEDLINE=9019050; PubMed=2628730;
MEDLINE=90190650; PubMed=2628730;
Moses H.L., Derynck R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   231 --TLHVEINGFNS---GRRGDLATIHGM--NRPFLLLMATPLERAQH--LHSSRHRRALD
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(Rel. 15, Last sequence update)
(Rel. 41, Last annotation update)
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letazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
letazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                (See http://www.isb-sib.
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EMBL; M32745; AAA40422.1;

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Search completed: April 15, 2003, 11:58:53 Job time: 23 secs
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PIR; A61039; A61039.

HSSP; P10600; ITGJ.

MGD; MGI:98727; T9fb3.

InterPro; IPR002400; GF_Cysknot.

InterPro; IPR003911; TGF_TGFb.

InterPro; IPR001839; TGFb.

InterPro; IPR001839; TGFb.

InterPro; IPR001111; TGFb.

Pfam; PF00019; TGF-beta; I...

Pfam; PF00688; TGFb_propeptide; 1...

PFINTS; PR00438; GFCYSKNOT.

PRINTS; PR01423; TGFBFA.

PRODOM; PD000357; TGF-BFTA.

PROSITE; PS00226; TGF-BFTA.; 1...

SMART; SM00204; TGFB; 1...

PROSITE; PS00250; TGF_BETA.; 1...
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                                                                                                                                                                                                                                                                                                                                                                                         179 WRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAH------SSSDSKDN- 230
                                                                                                                                                                                                                                                              346 CPYLRSADTTHSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVK 405
                                                                                                                                                                                                                                                                                                343 CPYIWSLDTQYSKVLALYNQHNPGASAAPÇCVPQALEPLPIVYYVGRKPKVEQLSNMIVR 402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    231 --TLHVEINGFNS---GRRGDLATIHGM---NRPFLLLMATPLERAQHLHSSRHRRALDT 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 QRYIGGKNLPTRGTAEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNGDILENV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 ITSKVFR-FNVSSVEK----NGTNLFRAEFRVLRVPNPSSKRTEQRIELFQILRPDEHIAK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127 TPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL----KLKVEQHVELYQKYSND----S 178
                                                                                                                                 406 SCKCS 410
                                                                                                                                                                                              403 SCKCS 407
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44.2%; Pred. No. 7.6e-59;
tive 57; Mismatches 127; Indels 53; Gaps
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N-LINKED (GLCNAC. . .) (POTENTIAL).

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CELL ATTACHMENT SITE (POTENTIAL).
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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     Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
Score
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Match
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Gapop 10.0 , Gapext 0.5
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TIANGE TO A TO	GDVPPGPL	ALIATICY 30.18; CONSERVATIVE LRLLPLLLPLLWLLVLJ	liminary; tra De: mRNA 390 <kon> ances: GB:M23 TGF-beta-1 : inhibin cowth factor</kon>	le type: protein ss; 279-322 cCHE> ah, P.; Van obberghen-Sc Chem. 263, 18313-18317, cDNA cloning of porcine nce number: 146657; MUID	A; Accession: A27314 A; Molecule type: mRNA A; Residues: 1-390 <der> R; Chaifetz, S; Weatherbee, Cell 48, 409-415, 1987 A; Title: The transforming gr A; Reference number: A90890; A.Accession: A26356</der>	transforming growth factor beta-1 p. N;Alternate names: TGF-beta (doc) (Species: Sus scrofa domestica (doc) (Species: Sus scrofa domestica (doc) (Date: 05-Jun-1988 #sequence_revis (;Accession: A27512; A26356; I46657 R;Derynck, R.; Rhee, L. Richer (Acids Res. 15, 3187, 1987 Nucleic Acids Res. 15, 3187, 1987 A;Teitle: Sequence of the porcine transference number: A27512; MUID:87		112.3 111.8 111.7 111.7 111.7 111.7 111.7 111.7 111.3 111.3 111.3 111.3 111.3 111.3 111.3
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YEART I A DOCCORNI CEDIMONYANA TECEPA TECEPA GARGGGGGKINNT HVET NGEN	SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 	PIEU. NO. 0.3E-130; 0: Mismatches 130; PGRPAAGLSTCKTIDMELVKRKR	id from GB/EMBL/DDBJ IID:9755044; PIDN:AAA6461 Score 2033.5; DB 2; Brod No 6 33-156.	n-Schilling, E.; Ludwig, R.L.; 1317, 1988 ceine transforming growth factor MUID:89054010; PMID:2461367	J.A.; Tsang, M.L.S.; Anderson, J owth factor-beta system, a compl MUID:87102890; PMID:2879635	recursor - pig mestic pig) ion 05-Jun-1988 #text. ion growth fact 174844; PMID:3470708	ALIGNMENTS	B40905 BMIU6 JH0688 JC4862 J45355 JH0687 BMIU2 A54798 S37073 A343918 JC5241 I45056 I45056 I45056 JC4151 JC4151
VELYOKYSNDSWR 180	VTRVLMVESGNQI 120	Indels 17; Gaps 1; IEAIRGQILSKLRLA 60	6.1; PID:g755045 Length 390;	Dhar, R.; Sporn, M.B.; pr-beta 1 mRNAs. Evidence	J.K.; Mole, J.E.; Luc	_change 16-Jul-1999 tor-beta precursor.		inhibin beta-A cha bone morphogenetic bone morphogenetic activin beta-A cha bone morphogenetic bone morphogenetic bone morphogenetic bone morphogenetic core treated prote bone bone morphogenetic rGF-beta-related pactivin beta E cha osteogenic protein bone morphogenetic bone morphogenetic bone morphogenetic activin beta D cha osteogenic protein bota D cha osteogenic protein
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transforming growth factor beta-1 - sheep (;Species: Ovis orientalis aries, Ovis ammon aries C;Date: 19-Dec-1997 #sequence_revision 19-Dec-1997 C;Accession: 140463; S45115 R;Wooddall, C.J.; McLaren, L.J.; Watt, N.J.
                                                                                   RESULT 3
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C:Species: Gallus gallus (chicken)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 24-Nov-1999
C:Accession: S01413
R:Jakowlew, S.B.; Dillard, P.J.; Sporn, M.B.; Roberts, A.B.
Nucleic Acids Res. 16, 8730, 1988
A:Title: Nucleotide sequence of chicken transforming growth factor-beta 1 (TGF-beta A:Reference number: S01413; MUID:88335639; PMID:3166520
A:Accession: S01413
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C;Superfamily: inhibin
C;Keywords: growth factor
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McLaren, L.J.; Watt, N.J
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transforming growth factor beta-1 precursor [validated] - human N;Alternate names: growth-inhibitory factor; TGF type 2; TGF-beta C;Species:.Homo sapiens (man) C;Date: 28-Feb-1986 #sequence_revision 19-Oct-1995 #text_change 08-Dec-2000 C;Accession: A27513; A01395; A22290; I59664; S53444 R;Derynck, R; Rhee, L; Chen, E;Y; Van Tilburg, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X76916; NID:g496648; PIDN:CAA54242.1; PID:g496649 A;Note: submitted to the EMBL Data Library, December 1993 C;Superfamily: inhibin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-390 < WOO>
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A;Title: Sequence and chromosomal localisation of the gene A;Reference number: I46463; MUID:95121932; PMID:7821809
A;Accession: I46463
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89.7%;
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Pred. No. 1.5
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factor-beta precursor

Nucleic Acids Res. 15, 3188-3189, 1987

A,Title: Intron-exon structure of the human transforming A, Reference number: A27513; MUID:87174845; PMID:3470709

A; Accession: A27513
A; Molecule type: DNA
A; Residues: 1-390 <DER> Nature 316, 701-705, 1985
A;Title: Human transforming growth factor-beta complementary DNA sequence and express A:Reference number: A01395; MUID:85296301; PMID:3861940
A;Accession: A01395 R; Derynck, R.; Jarrett, J.A.; Chen, A; Residues: 1-390 < DER> A; Cross-references: GB:X05839; GB:Y00112; E.Y.; NID:g37097; PIDN:CAA29283.1; PID:g1212989 Eaton, D.H.; Bell, J.R.; Assoian, Rob

A; Molecule type: mRNA
A; Residues: 1-9, 'p', 11-24, 'p', 26-159, 'R', 160-390 <DE2>
A; Cross-references: GB: X02812; GB: J05114; NID: g37092; PIDN: CAA2
A; Note: the authors suggest that residues 8-23 could represent
R; Massague, J.; Like, B.
J. Biol. Chem. 260, 2636-2645, 1985
A; Title: Cellular receptors for type beta transforming growth fa; Reference number: A22290; MUID: 85131019; PMID: 2982829
A; Accession: A22290 PIDN:CAA26580.1; represent the hydr hydrophobic PID:g37093 core

factor. Ligand binding

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A;Molecule type: protein
A;Residues: 279-295,'XX',298-301 <MAS>
R;Urushizaki, Y.; Niitsu, Y.; Terui, T.; Koshida, Y.; Mahara, K.; Kohgo, Y.; Urushizaki,
Tumor Res. 22, 41-55, 1987
A;Title: Cloning and expression of the gene for human transforming growth factor-beta in
A;Reference number: 159664
A;Accession: 159664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A:Cross-references: GDB:120729; OMIM:190180

A:Map position: 19q13.2-19q13.2

C:Superfamily: inhibin

C:Keywords: glycoprotein; growth factor; homodimer; mitogen; transformation

F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-278/Domain: propeptide #status predicted <PRO>
F:29-278/Domain: propeptide #status predicted <PRO>
F:244-246/Region: cell attachment (R-G-D) motif
F:279-390/Product: transforming growth factor beta-1 #status experimental <MAT>
F:82,136,176/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Stam, K.; Stewart, A.A.; Qu, G.Y.; Iwata, K.K.; Fenyoe, D.; Chait, B.T.; Marshak, D.R. Biochem. J. 305, 87-92, 1995
A;Title: Physical and biological characterization of a growth-inhibitory activity purifi A;Reference number: S53444; MUID:95126934; PMID:7826358
A;Accession: S53444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:M38449; NID:g339557; PIDN:AAA36735.1; PID:g339558
R;Stam, K.; Stewart, A.A.; Qu, G.Y.; Iwata, K.K.; Fenyoe, D.; Chait, B.T.; Marshak, D.R.
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A; Residues: 279-390 < RES>
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transforming growth factor beta-1 precursor - green monkey C:Species: Cercopithecus aethiops (green monkey, grivet) C:Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 24-Nov-1999 C:Accession: A26960 R:Sharples, K: Plowman, G.D.; Rose, T.M.; Twardzik, D.R.; Purchio, A.F. DNA 6, 239-244, 1987
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                                                                                                                                                                                                                                                                                                                                                                                                                        NOHNDGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
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A;Title: Cloning and sequence analysis of simian transforming growth factor-beta cDNA A;Reference number: A26960; MUID:87246074; PMID:3474130 A;Accession: A26960
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C;Superfamily: inhibin
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A; Residues: 1-390 <SHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transforming growth factor beta-1 - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 24-Nov-1999
C;Accession: JC4023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Cloning of a canine cDNA homologous to the human transforming growth factor-A;Reference number: JC4023; MUID:95237630; PMID:7721110 A;Accession: JC4023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Manning, A.M., 1995
                                                                                                                                                                                                                                         C;Superfamily: inhibin C;Keywords: growth factor; transforming protein F;288-390/Product: transforming growth factor beta 1 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-390 <MAN>
A;Residues: 1-390 <MAN>
C;Comment: This factor plays a multifunctional role as a regulator of mammalian cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNNSWR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
                                                                                                                                                       Local Similarity
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MPPSGLRLLPLLLPLLRLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLS 60
                                  WAPSGLKLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKKKRIEAIRGQILSKLRLA 60
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                                                                                                                              Conservative
                                                                                                                                                    87.7%; Score 1893.5; DB 2
88.7%; Pred. No. 1.2e-144;
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                                                                                                                              12; Mismatches
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A;Note: the authors suggest that residues 8-23 could represent the hydrophobic core of a C;Comment: The mature protein is the carboxyl-terminal segment of a precursor polypeptic C;Superfamily: inhibin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Derynck, R; Jarrett, J.A.; Chen, E.Y.; Goeddel, D.V.
J. Biol. Chem. 261, 4377-4379, 1986
A;Title: The murine transforming growth factor-beta precursor.
A;Reference number: A01396; MUID:86168129; PMID:3007454
A;Accession: A01396.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transforming growth factor beta-1 precursor - mouse N;Alternate names: TGF type 2; TGF-beta C;Species: Mus musculus (house mouse)
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A; Residues: 1-390 <DER>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change
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                                   241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNSYPYDVPDYASLALDTN 300
                                                                                                          181
                                                                                                                  181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
                                                                                                                                                                           121 YEKTKDISHSIYMFFNTSDIREAVPEPPLLSRAELRLQRLKSSVEQHVELYQKYSNNSWR 180
                                                                                                                                                                                                              121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLKLKVEQHVELYQKYSNDSWR 180
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                                                                                                                                                                                                                                                                                            61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
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                      PKRRGDLGTIHDMNRPFLLLMATPLERAQHLHSSRHRR---
                                                                                              YLGNRLLTPTDTPEWLSFDYTGVVRQWLNQGDGIQGFRFSAHCSCDSKDNKLHVEINGIS 240
                                                                                                                                                                                                                                                                                                                                      MPPSGLRLLPLLLPLPWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNSYPYDVPDYASLALDTN 300
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A; Residues: 1-390 < QIA>
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N;Alternate names: TGF type 2; TGF-beta
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346;
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C;Keywords: glycoprotein; growth factor; integrin binding F;l-29/Domain: signal sequence #status predicted <SIG>F;l-29/Domain: propeptide #status experimental <PRO>F;30-278/Domain: propeptide #status experimental <PRO>F;244-246/Region: cell attachment (R-G-D) motif F:279-390/Product: transforming growth factor beta-1 #status predicted <MAT>
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 24-Nov-1999
C;Accession: S10219; PT0023; S02267
R;Olan, S.W.; Kondalah, P.; Roberts, A.B.; Sporn, M.B.
Nucleic Acids Res. 18, 3059, 1990
A;Title: cDNA cloning by PCR of rat transforming growth factor beta-1.
A;Reference number: S10219; MUID:90272425; PMID:2349108
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A; Residues: 30-32,'X',34-38,'Q',40-42,'X',44 <OKA>
R; Okada, F; Yamaguchi, K; Ichihara, A.; Nakamura, T.
FEBS Lett. 242, 240-244, 1989
A; Title: One of two subunits of masking protein in latent TGF-beta
A; Reference number: S02267; MUID:89121078; PMID:2914605
A; Accession: S02267
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J. Biochem. 106, 304-310, 1989
A;Title: Purification and structural analysis of a latent form of transforming growth A;Reference number: PT0023; MUID:90036779; PMID:2478527
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                                                                      241 PKRRGDLGTIHDMNRPFLLLMATPLERAQHLHSSRHRR------ALDTN
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YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY
                                                                                                                                             SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNSYPYDVPDYASLALDTN 300
                                                                                                                                                                                                                   YLGNRLLTPTDTPEWLSFDVTGVVRQWLNQGDGIQGFRFSAHCSCDSKDNVLHVEINGIS 240
                                                                                                                                                                                                                                                                                  YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
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85.0%; Pred. No. 5.5e-140;
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transforming growth factor beta-1 precursor - bovine (fragment)
N;Alternate names: beta-TGE; cartilage-inducing factor-A; EGF-dependent TGF or dEGF; MGF
C;Species: Bos primigenius taurus (cattle)
C;Bete: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 16-Jul-1999
C;Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 16-Jul-1999
C;Accession: A40057; A4230; A05284; A24322; B61439
R;Van Obberghen-Schilling, E.; Kondaiah, P.; Ludwig, R.L.; Sporn, M.B.; Baker, C.C.
Mol. Endocrinol. 1, 693-698; 1987
A;Title: Complementary decxyribonucleic acid cloning of bovine transforming growth factor A;Reference number: A40057; MUID:91042552; PMID:3153459
A;Accession: A40057; MUID:91042552; PMID:3153459
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A; Residues: 204-218 (ROB>
A; Residues: 204-218 (ROB>
A; Residues: 204-218 (ROB>
A; Residues: 204-218 (ROB>
A; Residues: 261, 5693-5695, 1986

J. Biol. Chem. 261, 5693-5695, 1986
J. Biol. Chem. 261, 5693-5695, 1986
A; Title: Cartilage-inducing factor-A. Apparent identity to transforming growth factor-be
A; Reference number: A24322; MUID:86195954; PMID:3754555
A; Accession: A24322
A; Molecule type: protein
A; Residues: 204-233 (SEY>
A; Rolecule type: protein
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A;Residues: 204-209,'X',211-217 <OGA>
R;Residues: 204-209,'X',211-217 <OGA>
R;Roberts, A.B.; Anzano, M.A.; Meyers, C.A.; Wideman, J.; Blacher, R.; Pan, Y.C.E.; Stein Blochemistry 22, 5692-5698, 1983
Blochemistry 22, 5692-5698, 1983
A;Title: Purification and properties of a type beta transforming growth factor from bovin A;Reference number: A05284; MUID:84104793; PMID:6607069
A;Accession: A05284
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A;Title: Purification and characterization of transforming growth factor-beta2.3 and -beta-ference number: A42320; MUID:92129307; PMID:1733936
A;Accession: A42320
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Protein Chem. 10, 565-575, 1991
A;Title: Separation, purification, and sequence identification of TGF-betal and TGF-beta A;Reference number: A61439; MUID:92189724; PMID:1799413
A;Accession: B61439
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A;Molecule type: protein
A;Residues: 204-209; X',211-217, 'XX',220-232 <JIN>
C;Comment: This polypeptide is composed of two polypeptide chains cross-linked by disulf C;Comment: Type II TGF does not bind to the EGF receptor and lacks intrinsic mitogenic a C;Comment: Type II TGF does not bind to the EGF receptor and lacks intrinsic mitogenic a con. Cells grown in monolayer do not respond in a similar manner to these growth factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C:Keywords: glycoprotein; growth factor; heterodimer F;204-315/Product: transforming growth factor beta-1 #status experimental <MAT>F;7,61,101/Binding site: carbohydrate (Asn) (covalent) #status predicted
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   121
                                                           196 LSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFNSGRRGDLATIHGMNR 255
                                                                                                                61 NTSELREAVPEPVLLSRADVRLLRLKLKVEQHVELYQKYSNNSWRYLSNRLLAPSDSPEW 120
                                                                                                                                                                                                                                       1 AILALYNSTRDRVAGESAETEPEPEADYYAKEVTRVLMVEYGNKIYDKMKSSSHSIYMFF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 407
                                                                                                                                                                                                                                                                                                   AVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQIYDKFKGTPHSLYMLF 135
NTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWRYLSNRLLAPSDSPEW 195
                                                                                                                                                                                                                                                                                                                                                                 295;
                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                          72.8%;
88.9%;
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                                                                                                                                                                                                                                                                                                                                                                                          Score 1572.5; DB 2; Pred. No. 6.1e-119;
                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                    Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                          Length 315;
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A41918
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A; Residues: 1-373 <BUR>
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C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
C;Accession: A41918; A34941; S03110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       376 QALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 407
                                           317 IDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQ 376
                                                                                                                                                                                                                              181
                                                                                                                                                                                                                                                                                   204 VRQWLTRREAIEGFRLSAHSSSD----SKDNTLHVEINGFNSGRRGDLATIHGMNR--PFL 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 QRARLRPPPDGPDEYWAKELRRIPMETTWDGAMEHWQPQSHSIFFVFNVSRARRG-GRPT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 LSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVPPGPLPEAVLALYNSTRDRVA 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90 GES-VEPEPEPEADYYAKEVTRVLMVESGNQIYDKFKGTPHSLYMLFNTSELREAVPEPV 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                             LAMALPAERANELHSARRR---
                                                                                                                                                               LLMATPLERAQHLHSSRHRRALDTNSYPYDYPDYASLALDTNYCF--SSTEKNCCVRQLY 316
                                                                                                                                                                                                                        VHQWLSGSELLGVFKLSVHCPCEMGPGHAEEMRISIEGFEQ-QRGDMQSIAKKHRRVPYV 239
                                                                                                                                                                                                                                                                                                                                              LLHRAELRMLRQKAAADSAGTEQRLELYQGYGNASWRYLHGRSVRATADDEWLSFDVTDA 180
                                                                                                                                                                                                                                                                                                                                                                                                    LLSRAELRLLRLKLK-----VEQHVELYQKYSNDSWRYLSNRLLAPSDSPEWLSEDVTGV 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSTCQRLDLEAAKKKRIEAVRGQILSKLRLTAPPPASETPPRPLPDDVRALYNSTQELLK 61
            207;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48.5%; Score 1047; DB 2; 52.9%; Pred. No. 1.6e-76;
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A:Residues: 173-322, ELPT', 327-412 <BU3>
A:Residues: 173-322, ELPT', 327-412 <BU3>
A:Cross-references: EMBL:X60091
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1991
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1991
MO1. | Endocrinol. 6, 1285-1298, 1992
MO1. | Endocrinol. 6, 1285-1298, 1992
A:Title: Identification and characterization of the Chicken transforming growth factor-la:Reference number: I51181; MUID:93024487; PMID:1406706
A:Accession: I51181
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A; Residues: 1-117 <JA2>
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A;Residues: 119-172 <BU2>
A;Residues: 119-172 <BU2>
A;Cross-references: EMBL:X60055; NID:g396688; PIDN:CAA42653.1; PID:g396689
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1991
A;Accession: S36124
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R;BuTt, D.W.; Paton, I.R.; Dey, B.R.
J. Mol. Endocrinol. 7, 175-183, 1991
A;Title: Comparative analysis of human and chicken transforming growth factor-beta-2 and A;Reference number: $25850; MUID:92134496; PMID:1840616
A;Accession: $25850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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A;Accession: A34939
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A;Accession: S36125
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                     67
                                                                                                                                                                            15 LLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVPPGPLP 74
                                                        75 EAVLALYNSTRDRVAGESVEPEPE-----PEADYYAKEVTRVLMVE---SGNQIYDKF 124
                                                                                                                                                                                                                                                                                   Local
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                                                                                                                   9 LVLLSLLSFATVSLALSSCTTLDLEHIKKKRVEAIRGQILSKLRLTSPPE--SVGPAHVP 66
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YQILALYNSTRELL-.EEMEEEKEESCSQENTESEYYAKEIHKFDMIQGLPEHNELGICP 124
                                                                                                                                                                                                                                                          198;
                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                             40.48;
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                                                                                                                                                                                                                                                                             Score 871.5;
Pred. No. 2.5
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                                                                                                                                                                                                                                                                                                      Length 412;
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C;Keywords: growth factor
F;271-382/Product: transforming growth factor beta-5 #status experimental <MAT>
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A; Residues: 271-276,'x',278-284,'xx',287-299 <ROB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A:Cross-references: GB:J05180; NID:g214821; PIDN:AAA49968.1; PID:g214822 R;Roberts, A.B.; Rosa, F.; Roche, N.S.; Coligan, J.E.; Garfield, M.; Rebbert, M.L.; K Growth Factors 2, 135-147, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: B61036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Title: Isolation and characterization of TGF-beta2 and TGF-beta5 from medium condit A; Reference number: A61036; MUID:90253806; PMID:2340184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transforming growth factor beta-5 precursor - African clawed frog C; Species: Xenopus laevis (African clawed frog) C; Date: 31-Dec-1993 #sequence_revision 03-Feb-1994 #text_change 16-Jul-1999 C; Accession: A34929; B61036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-382 <KOI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Biol. Chem. 265, 1089-1093, 1990
A;Title: Identification of a novel transforming growth factor-beta (TGF-beta5) mRNA i A;Reference number: A34929; MUID:90110090; PMID:2295601
A;Accession: A34929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Kondaiah, P.;
J. Biol. Chem.;
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      236 INGFNSGRRGDLATIHGM--NRPFLLLMATPLERAQHLHSSRHRRALDTNSYPYDVPDYA 293
                                                              171 SRYLESKYITPYTDDEWMSFDYTKTVNEWLKRAEENEQFGLQPACKCPTPQAKD----ID 226
                                                                                                                          180 -RYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAH---SSSDSKDNTLHVE 235
                                                                                                                                                                                                        116
                                                                                                                                                                                                                                          124 FKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKL--KVEQHVELYQKYSNDSW-- 179
                                                                                                                                                                                                                                                                                                      60 EKMTVPSEAIFLYNSTLEVIREKATREEEHVGHDQNIQDYYAKQVYR---FESITELED- 115
                                                                                                                                                                                                                                                                                                                                                                 69 PPGPLPEAVLALYNSTRDRVAGESVEPE-----PEPEADYYAKEVTRVLMVESGNQIYDK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          404 MVVKSCKCS 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   399 MIVRSCKCS 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              344 CSGPCPYLRSADTTHSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    339 CLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSN 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 NLHEVLEIKFKGIDSEDDYGRGDLGRLKKQKDLHNPHLILMMLPPHRLESPTLGGQRKKR
                                                                                                                                                                                                                                                                                                                                                                                                                             1 MEVLWMLLVLLVLHLSSLAMSLSTCKAVDMEEVRKRRIEAIRGQILSKLKLDKTPDV-DS 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 LPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDV 68
                                                                                                                                                                                  -----HEFKFKENASHVRENVGMNSLLHHAELRMYKKQTDKNMDQRMELFWKYQENGTTH 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N---TLHVEINGFNSG---RRGDLATI---HGMNRPFLLLMATPLERAQH--LHSSRHRR 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAH-----SSSDSKD 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL----KLKVEQHVELYQKYSND--- 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALDTNSYPYDVPDYASLALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANF 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KGVTSNVFR-ENVS---SAEKNSTNLFRAEFRVLRVPNPSSKRSEQRIELFQILRPDEHI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1-382 <KON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40.2%; Score 868.5; DB 2
45.9%; Pred. No. 3.9e-62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 382;
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47;

Gaps

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transforming growth factor beta-3 precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999
C;Accession: S01825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Derynck, R.; Lindquist, P.B.; Lee, A.; Wen, D.; Tamm, J.; Graycar, J.L.; Rhee, EMBO J. 7, 3737-3743, 1988
A;Title: A new type of transforming growth factor-beta, TGF-beta3.
A;Reference number: S01824; MUID:89091120; PMID:3208746
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F;26-297/Domain: propeptide #status predicted <PRO>
F;298-409/Product: transforming growth factor beta-3 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X14150; NID:g2127; PIDN:CAA32363.1; PID:g2128 C;Superfamily: inhibin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-409 < DER>
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transforming growth factor beta-3 precursor - mouse
C; Species: Mus musculus (house mouse)
C; Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAH-----SSSDSKDN- 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TPHSLYMLENTSELREAVPEPVLLSRAELRLLRL----KLKVEQHVELYQKYSND----S 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TQVLDLYNSTRELLEEVHGERGDDCTQENTESEYYAKEIYKFDMIQGLEEHNDLAVCPKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EAVLALYNSTR---DRVAGESVE--PEPEPEADYYAKEVTRVLMV---ESGNQIYDKFKG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LVVLALLNFATVSLSMSTCTTLDFDHIKRKRVEAIRGQILSKLRLTSPPDPSML--ANIP 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVPPGPLP 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                QEVMEIKFKGVDSEDDPGRGDLGRLKKKKEHSPHLILMMIPPDRLDNPGLGAQRKKR----
                                                                                                                                                                                                                     RSCKCS 407
                                                                                                                                                                                                                                                                                                                                                                                         TNSYPYDVPDYASLALDINYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --TLHVEINGFNS---GRRGDLATIHGM--NRPFLLLMATPLERAQH--LHSSRHRRALD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QRYIDGKNLPTRGAAEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNGDILENI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ITSKIFR-FNVSSVEK---NETNLFRAEFRVLRMPNPSSKRSEQRIELFQILQPDEHIAK 180
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                                                                                                                                                                       KSCKCS 409
                                                                                                                                                                                                                                                                  PCPYLRSADTTHSSVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTAKVEQLSNMVV
                                                                                                                                                                                                                                                                                                                PCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIV 401
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                                                                                                                                                                                                                                                                                                                                                                ~----ALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSG
     #sequence_revision 03-Apr-1992 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38.6%;
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Pred. No. 2.6e-59;
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A;Molecule type: mRNA
A;Residues: 1-410 < DEN>
A;Residues: 1-50 < DEN>
R;Watrin, F.; Scotto, L.; Assoian, R.K.; Wolgemuth, D.J.
Cell Growth Differ: 2, 77-83, 1991
Cell Growth Differ: 2, 77-83, 1991
A;Title: Cell lineage specificity of expression of the murine transforming growth fac
A;Reference number: A61225; MUID:91299576; PMID:2069871
A;Accession: A61225
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A;Residues: 1-410 <MIL>
A;Residues: 1-410 <MIL>
A;Residues: 1-410 <MIL>
A;Cross-references: GB:M32745; NID:g201949; PIDN:AAA40422.1; PID:g201950
A;Cross-references: GB:M32745; NID:g201949; PID:g201949; PID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Superfamily: inhibin
C;Keywords: glycoprotein; growth factor; growth regulation
C;Keywords: glycoprotein; growth factor; growth regulation
F;1-21/Domain: signal sequence #status predicted <SIG>
F;2-298/Domain: propeptide #status predicted <PRO>
F;25-261/Region: cell attachment (R-G-D) motif
F;299-410/Product: transforming growth factor beta-3 #status predicted <MAT>
F;299-410/Product: transforming growth factor beta-3 #status predicted <MAT>
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A; Residues: 285-410 <WAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Growth Factors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Complementary DNA cloning of the murine transforming growth factor-beta3 (TG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; Miller, D.A.; Lee, A.; Matsui, Y. Mol. Endocrinol. 3, 1926-1934, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: A41397; A61039; A61225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Вþ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: translation not shown
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                                                                                    δõ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179 WRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAH-----SSSDSKDN- 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125 ITSKVFR-FNVSSVEK---NGTNLFRAEFRVLRVPNPSSKRTEQRIELFQILRPDEHIAK 180
                                                                                                                                                                                             406
                                                                                              403 SCKCS 407
                                                                                                                                                                                                                                                                                           343 CPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVR 402
                                                                                                                                                                                                                                                                                                                                                                                               297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 HEVMEIKFKGVDNEDDHGRGDLGRLKKQKDHHNPHLILMMIPPHRLDSPGQGSQRK----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QRYIGGKNLPTRGTAEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNGDILENV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TPHSLYMLENTSELREAVPEPVLLSRAELRLLRL----KLKVEQHVELYQKYSND----S 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EAVLALYNSTR----DRVAGESVE---PEPEPEADYYAKEVTRVLMVE----SGNQIYDKFKG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LVVLALLNLATISLSLSTCTTLDFGHIKKKRVEAIRGQILSKLRLTSPPEPSVMT--HVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YQVLALYNSTRELLEEMHGEREEGCTQETSESEYYAKEIHKFDMIQGLAEHNELAVCPKG 124
                                                                                                                                                                                                                                                                                                                                                                                               -----KRALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --TLHVEINGENS----GRRGDLATIHGM---NRPFLLLMATPLERAQHLHSSRHRRALDT 282
SCKCS 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NSYPYDVPDYASLALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         188;
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44.2%; Pred. No. 8.6
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RESULT 15 A55706 transforming

growth factor beta-3 precursor

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Search completed: April 15, 2003, 12:01:18 Job time : 39 secs
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C;Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 16-Jul-1999
C;Adcession: A55706; B40699; S36042
R;Wang, J; Kuliszewski, M; Yee, W.; Sedlackova, L.; Xu, J; Tseu, I.; Post, M.
J. Biol. Chem. 270, 2722-2728, 1995
A.Title: Cloning and expression opf
A;Reference number: A55706; MUID:95155340; PMID:7852342
A;Accession: A55706; MUID:95155340; PMID:7852342
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A;Residues: 157-211 <MCK>
A;Residues: 157-211 <MCK>
C;Superfamily: inhibin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:U03491
A;Note: it is uncertain whether Met-1 is the initiator
R;McKinnon, R.D.; Piras, G; Ida Jr., J.A.; Dubois-Dalcq, M.
J. Cell Biol. 121, 1397-1407, 1993
A;Title: A role for TGF-beta in oligodendrocyte differentiation.
A;Reference number: A40699; MUID:93286190; PMID:8509457
A;Accession: B40699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-410 <WAN>
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                                                                                                                             403 SCKCS 407
                                                                                                                                                                                                                                                  241 HEVMEIKFKGVDNEDDHGRGDLGRLKKQKDHHNPHLILMMIPPHRLDSPGQGGQRK---- 296
                                                                                                                                                                                                                                                                                                                                                                                                                         406 SCKCS 410
                                                                                                                                                               343 CPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVR 402
                                                                                                                                                                                                                                                                                                                                                                               231 --TLHVEINGFNS---GRRGDLATIHGM---NRPFLLLMATPLERAQHLHSSRHRRALDT 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    127 TPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL----KLKVEQHVELYQKYSND----S 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 YQVLALYNSTRELLEEMHGEREEGCTQETSESEYYAKEIHKFDMIQGLAEHNELAVCPKG 124
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Minimum
Maximum
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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1: /cgn2_6/ptodata/1,
2: //gn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
5: //gn2_6/ptodata/1,
5: //gn2_6/ptodata/1,
6: //gn2_6/ptodata/1,
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2159
1 MAPSGLRLLPLLLPLI
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US-08-35-939A-2

PCT-US94-03705-6

PCT-US91-01861-2

US-08-132-405-4

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US-08-939-393A-4

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US-09-380-662-21
PCT-US91-04541-2
  US-08-065-844A-8
US-07-979-441-1
US-08-197-792-36
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US-08-132-405-1
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Sequence 21, A	Sequence 23, A	Sequence 23, A	Sequence 21, A	Sequence 22, A	Sequence 21, A	Sequence 21, A	Sequence 23, A	Sequence 21, A	Sequence 23, A	Sequence 1, Ap	Sequence 30, A	Sequence 5, Ap	Sequence 2, Ap	Sequence 1, Appl	Sequence 41, A	Sequence 30, A	Sequence 36, A
Appl	App1	Appl	Appl	Appl	Appl	App1	App1	Appl	App1	Appli	Appl	Appli	pli	pli	App1	Appl	Appl

ALIGNMENTS

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                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/063841
FILING DATE: 18-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/790856
FILING DATE: 12-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/401906
FILING DATE: 01-SEP-1989
ATTORNEY/AGENT INFORMATION:
NAME: HASAK, Janet E.
REGISTRATION NUMBER: 28,616
REGISTRATION NUMBER: 597D1C:
TELECOMMUNICATION:
                                                    TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
LENGTH: 390 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb 1
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Anmann, Arthur J.
APPLICANT: Rudman, Christopher G.
TITLE OF INVENTION: Method of Ind
TITLE OF INVENTION: TGF-Beta
                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: C
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               TOPOLOGY:
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460 Point San Bruno Blvd
                                                        390 amino acids
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RESULT 2
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Patent No. 5604204
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                                                                                                                                                                                                                                                                                                                   ZIF: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FIRM PC PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ammann, Arthur J.
APPLICANT: Rudman, Christopher G.
FITLE OF INVENTION: TCR-BETA COMPOSITION FOR INDUCING BONE
FITLE OF INVENTION: GROWTH
                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/0
FILING DATE: 18-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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APPLICATION NUMBER:
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                     TTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                       APPLICATION NUMBER: 08/1
FILING DATE: 12-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
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                                     FILING DATE:
                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/395,939A
FILING DATE: 27-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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                                                                                           12-NOV-1991
                                       1-SEP-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application PC/TUS9101861 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
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TOPOLOGY: 1:00
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
               CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: 1
                                                                                                             SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch,
                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Genentech, Inc.
TITLE OF INVENTION: Method of Predisposing Mammals
TITLE OF INVENTION: Accelerated Tissue Repair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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                                                                        APPLICATION NUMBER: POFILING DATE: 19910320
                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                  STREET: 460 Point San Bruno Blvd CITY: South San Francisco
                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
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                                                                                           PCT/US91/0186
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                   No.
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ATTORNEY/AGENT INFORMATION: NAME: Hasak, Janet E.

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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 390 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                              SEQ ID NO:2
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Best Local :
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TELEPHONE: 415/266-1896
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 21 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: DERYNCK, RIK M.A.; GOEDDEL, DAVID V. TITLE OF INVENTION: NUCLEIC ACID ENCODING TGF-B ITS USES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
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                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 88.9%; Score 1919.5; DE Local Similarity 89.7%; Pred. No. 3e-169; es 365; Conservative 10; Mismatches 1
                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/07/389,929 FILING DATE: 04-AUG-1989
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                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                         LENGTH: 390
                                                                                             1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
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YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNNSWR 180
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                                                                         MPPSGLRLLPLLLPLLWLLVLTPGPPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
                                                                                                                                                 365;
                                                                                                                                               Conservative
                                                                                                                                                 88.9%; Score 1919.5; DB 6;
89.7%; Pred. No. 3e-169;
tive 10; Mismatches 15;
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US-07-669-171-2
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                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 390 amin
                                                                                                              Matches 364;
                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: PURCHIO, ANTHONY F.
APPLICANT: MADISEN, LINDA
APPLICANT: MERWIN, JUNE RAE
TITLE OF INVENTION: TGF-51/b2: A NOVEL CHIMERIC TRANSFORMING
TITLE OF INVENTION: GROWTH FACTOR-BETA
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 56:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 AVENUE OF THE AMERICAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA
                                                                                                                                                                                                           MOLECULE TYPE:
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STATE: N.Y.
COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 19910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 10036
                                                                                                                Match 88.7%; Score 1914.5; DB 1; Local Similarity 89.4%; Pred. No. 8.7e-169; nes 364; Conservative 10; Mismatches 16;
                                                                                                                                                                                                                             TOPOLOGY:
61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
                                   YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANECLGPCPYIWSLDTQYSKVLALY 360
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PCT-U$94-03705-5
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PCT-US94-03705-5
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      Best
                 Query Match
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                                                                                                                                        TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Mu-En Lee
APPLICANT: Mark A. Perrella
TITLE OF INVENTION: TRANSFORM
TITLE OF INVENTION: FACTOR-
TITLE OF INVENTION: SYNTHASE
TITLE OF INVENTION: TRANSCRIP
                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                               TELEPHONE: (617) 542-5070
TELEPHONE: (617) 542-8906
TELEPAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
CITY: BO
STATE: N
COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR------ALDTN
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                                                                            STRANDEDNESS:
                                                                                             TYPE:
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                                                               TOPOLOGY:
                                                                                                          LENGTH:
                                                                                                                                                                                                               NAME: Janis K. Fraser
REGISTRATION NUMBER: Reg
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 5 Apr
                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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   88.4%;
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                                                                                                                                                                                                    Reg. NO. 3.
AFR: 05433/007001
                                                                                                                                                                                                                                                                                                                                                      PCT/US94/03705
Score 1909;
Pred. No. 2.
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)9; DB 5;
2.8e-168;
            Length 394;
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US-08-132-405-3
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REFERENCE/DOCKET NUMBER: 59
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEPAX: 415/952-9881
                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/40
FILING DATE: 01-SEP-1989
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
                                                                                                                                                                                          FILING DATE: 18-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/7
                                                                                                                                                                                                                                                                                                        SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/1:
FILING DATE: 06-OCT-1993
                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ammann, APPLICANT: Rudman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                   NAME: Hasak, Janet I
REGISTRATION NUMBER:
                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
SOFTWARE: patin (
                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER:
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South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             California
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                                                                                                                                                                                                                                                                                                                                                                              IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                      INFU....
, Janet E.
- TTR: 28,616
597
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Method of Inc
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                                                                                                                                                                                                                                                                                                                                                                                                                  360 Kb floppy disk
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 412 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ammann, A
APPLICANT: Rudman, C
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 QRYIGGKNLPTRGTAEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNGDILENI 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127
                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            283 NSYPYDVPDYASLALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGP 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243 HEVMEIKFKGVDNEDDHGRGDLGRLKKQKDNNNPHLILMMIPPHRLDNPGQGGQRK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179 WRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAH-----SSSDSKDN- 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       408 SCKCS 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 LLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVPPGPLP 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 YQYLALYNSTRELLEEHGERKEEGCTQENTESEYYAKEIHKFDMIQGLAEHNELAVCPKG 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 LYVLALLNFATVSLSISTCTTLDFGHIKKKRVEAIRGQILSKLRLTSPPEPTVMT--HVP 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 38.4%; Score 828.5; DB 1; ocal Similarity 44.5%; Pred. No. 2.1e-68;
                                                      APPLICATION NUMBER: US/08/395,939A FILING DATE: 27-FEB-1995
                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL----KLKVEQHVELYQKYSND----S 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --TLHVEINGFNS---GRRGDLATIHGM---NRPFLLLMATPLERAQHLHSSRHRRALDT 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ITSKVFR-FNVSSVEK---NRTNLFRAEFRVLRVPNPSSKRNEQRIELFQILRPDEHIAK 182
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                                                                                                                                                                                                                   94080
                                                                                                                                                                                                                                                    South San Francisco 
: California
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460 Point San Bruno Blvd
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Christopher G.
TGF-BETA COMPOSITION FOR INDUCING BONE
    08/132405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57; Mismatches 126;
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                                                                                                                                                                                  RESULT 9
US-09-380-662-21
                                                                                                                  Sequence 21, Application US/09380662
Patent No. 6376199
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
               APPLICANT: Caniggia, Isabella
APPLICANT: Post, Martin
APPLICANT: Lye, Stephen
TITLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF TROPHOBLAST
FILE REFERENCE: 11757.38USWO
FILE REFERENCE: 1257.38USWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415,952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
CURRENT APPLICATION NUMBER: US/09/380,662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 07/4(FILING DATE: 1-SEP-1989ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                     348 CPYLRSADTTHSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVK 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243 HEVMEIKFKGVDNEDDHGRGDLGRLKKQKDNNNPHLILMMIPPHRLDNPGQGGQRK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 231 --TLHVEINGFNS---GRRGDLATIHGM---NRPFLLLMATPLERAQHLHSSRHRRALDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 QRYIGGKNLPTRGTAEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNGDILENI 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 ITSKVFR-FNVSSVEK---NRTNLFRAEFRVLRVPNPSSKRNEQRIELFQILRPDEHIAK 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 412 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                        408 SCKCS 412
                                                                                                                                                                                                                                                                                                                 403 SCKCS 407
                                                                                                                                                                                                                                                                                                                                                                               343 CPYIWSLDTQYSKVLALYNQHNDGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVR 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 TPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL----KLKVEQHVELYQKYSND----S 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 LLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVPPGPLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 YQYLALYNSTRELLEEHGERKEEGCTQENTESEYYAKE1HKFDMIQGLAEHNELAVCPKG 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 38.4%; Score 828.5; DB 1; Length 412; Local Similarity 44.5%; Pred. No. 2.1e-68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 LVVLALLNFATVSLSLSTCTTLDFGHIKKKRVEAIRGQILSKLRLTSPPEPTVMT--HVP 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NSYPYDVPDYASLALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGP 342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                             --KRALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGP
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RESULT 10
PCT-US91-04541-2
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-380-662-21
                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application PC/TUS9104541 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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PRIOR FILING DATE: 1997-03-07
NUMBER OF SEQ ID NOS: 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QURRENT FILING DATE:
                                                SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
                                                                                                                         MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                348 CPYLRSADTTHSTYLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVK 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    231 --TLHVEINGFNS---GRRGDLATIHGM---NRPFLLLMATPLERAQHLHSSRHRRALDT 282
CLASSIFICATION:
               APPLICATION NUMBER: FILING DATE: 19910
                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 QRYIGGKNLPTRGTAEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNGDILENI 242
                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                              ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCKCS 407
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                                                                                                                                                                  10112
                                                                                                                                                                                                                           New York
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                                                                                                                                                                                                                                                                                                         F: Oncogene Science Inc.
INVENTION: TISSUE DERIVED TUMOR GROWTH INHIBITORS
                                                                                                                                                                                                     New York
                                                                                                                                                                                                                                          30 Rockefeller Plaza
                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                   19910625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38.2%; Score 824.5; DB 4; Length 412; 44.2%; Pred. No. 4.8e-68; tive 58; Mismatches 126; Indels 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1999-12-21
                               PCT/US91/04541
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APPLICANT: IWATA, KENNETH K.; FOULKES, J.GORDON; DIJKE, ; PETER T.; HALEY, JOHN D.
TITLE OF INVENTION: METHOD FOR OBBTAINING BONE MARROW FREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qy
                                                                                                                                                                                                                                            ;OF TUMOR CELLS USING TRANSFORMING GROWTH FACTOR B3; NUMBER OF SEQUENCES: 9
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                                                                                                                                                                                                                                                                                                                                                        ;Patent No. 5262319
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                             APPLICATION NUMBER: US/V
FILING DATE: 25-JUN-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
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NAME: White, John P.
REGISTRATION'NUMBER: 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    403 SCKCS 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        343 CPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVR 402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 299
                                                                              APPLICATION NUMBER: 353,410
FILING DATE: 17-MAY-1989
APPLICATION NUMBER: 183,410
FILING DATE: 20-APR-1988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 WRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAH-----SSSDSKDN- 230
APPLICATION NUMBER: 922,121 FILING DATE: 20-OCT-1986
                                       APPLICATION NUMBER: 111,022 FILING DATE: 20-OCT-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183 QRYIGGKNLPTRGTAEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNGDILENI 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               127 TPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL----KLKVEQHVELYQKYSND----S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 LLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVPPGPLP 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CPYLRSADTTHSTYLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNNVVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NSYPYDVPDYASLALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGP 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --TLHVEINGFNS---GRRGDLATIHGM---NRPFLLLMATPLERAQHLHSSRHRRALDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ITSKVFR-FNVSSVEK----NRTNLFRAEFRVLRVPNPSSKRNEQRIELFQILRPDEHIAK 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----KRALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : (212)977-9550
(212)664-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38.2%; Score 824.5; DB 5; 44.2%; Pred. No. 4.8e-68;
                                                                                                                                                                                                         US/07/543,341
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PCT-US91-01861-3
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                                                                                                ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb fle
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/0186:
FILING DATE: 19910320
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Genentech, Inc.
TITLE OF INVENTION: Method of Predisposing Mammals to
TITLE OF INVENTION: Accelerated Tissue Repair
                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               127 ITSKVFR-FNVSSVEK---NRTNLFRAEFRVLRVPNPSSKRNEQRIELFQILRPDEHIAK 182
FILING DATE: 4 April 1990 ATTORNEY/AGENT INFORMATION:
                                                            CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        231 --TLHVEINGENS---GRRGDLATIHGM---NRPFLLLMATPLERAQHLHSSRHRRALDT 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183 QRYIGGKNLPTRGTAEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNGDILENI 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 WRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAH-----SSSDSKDN- 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127 TPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL----KLKVEQHVELYQKYSND----S 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                403 SCKCS 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 847,931
FILING DATE: 07-APR-1986
APPLICATION NUMBER: 725,003
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                                                                                                                                                                                                                                                                                                                            STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                             STATE:
                                        APPLICATION NUMBER: U.S. Ser. No. 07/504,495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NSYPYDVPDYASLALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGP 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HEVMEIKFKGVDNEDDHGRGDLGRLKKQKDHHNPHLILMMIPPHRLDNPGQGGQRK----
                                                                                                                                                                                                                                                                                                             California
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                                                                                                                          PCT/US91/01861
                                                                                                                                                                                                                           360 Kb floppy disk
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US-08-132-405-2
; Sequence 2, Application US/08132405
; Patent No. 5409896
; GENERAL INFORMATION:
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Best Local S
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SEQUENCE CHARACTERISTICS:
LENGTH: 410 amino acids
TYPE: AMINO ACID
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TELEPHONE: 415/266-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NERAL LMTONAMENT ARTHOUGH. APPLICANT: Ammann, Arthough.
APPLICANT: Ammann, Christopher G.
APPLICANT: Rudman, Christopher G.
APPLICANT: Rudman, Christopher G.
TITLE OF INVENTION: Method of Inducing Bone Growth Using
TITLE OF THE OF TH
                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                346 CPYLRSADTTHSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVK 405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 WRYLSNRLLAPSDSPEWLSEDVTGVVRQWLTRREAIEGFRLSAH------SSSDSKDN- 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                343 CPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVR 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       406 SCKCS 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Hasak, Janet 1 REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 LLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVPPGPLP 74
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Local Similarity 44.2%; Pred. No. 5.9e-68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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                                                                                                                                                                                                                                                                                       CITY: South San Francisco
STATE: California
                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NSYPYDVPDYASLALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGP 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----KRALDINYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGP
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                                                                                                                                                                                                            94080
                                                                                                                                                                                                                                                                                                                                                                     E: Genentech, Inc.
460 Point San Bruno Blvd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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patin (Genentech)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28,616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126;
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RESULT 14
US-08-395-939A-2
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                                                                  Sequence 2, Application US/08395939A
Patient NO. 5604204
GENERAL INFORMATION:
APPLICANT: Anmann, Arthur J.
APPLICANT: Rudman, Christopher G.
TITLE OF INVENTION: TGF-BETA COMPOSITION FOR INDUCING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 414 amin
                                                        TITLE OF INVENTION:
                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 07/401906
FILING DATE: 01-SEP-1989
ATTORNEY/AGENT INFORMATION:
NAME: HASAK, JANGE E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 597D:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/063841
FILING DATE: 18-MAY-1993
                                                                                                                                                                                                                                                              356 SDTQHSRVLSLYNTINPEASASPCCVSQDLEPLTILYYIGKTPKIEQLSNMIVKSCKCS 414
                                                                                                                                                                                                                                                                                    349 LDTQYSKVLALYNOHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 407
                                                                                                                                                                                                                                                                                                                                         303 -----ALDAAYCFRNVQDNCCLRPLYIDFKRDLGWKWIHEPKGYNANFCAGACPYLWS
                                                                                                                                                                                                                                                                                                                                                                           289 VPDYASLALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWS 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               189 PSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSS-----DSKDNTLHVE-- 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138 SELREAVPEPVLLSRAELRLLRL---KLKV-EQHVELYQ-----KYSNDSWRYLSNRLLA 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      236 -INGENSGRRGDLATIHGMNR-----PFLLLMATPLERAQHLHSSRHRRALDTNSYPYD 288
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  ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 AAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVP-PGPLPEAVLALYNSTR 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/132,405 FILING DATE: 06-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRAEGEWLSFDYTDAVHEWLHHKDRNLGFKISLHCPCCTFVPSNNYIIPNKSEELEARFA 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SAMEKNASN---LVKAEFRVFRLQNPKARVPEQRIELYQILKSKDLTSPTQRYIDSKVVK 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181;
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Genentech, Inc.
                                                        GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37.5%; Score 809; DB 1; Length 414; 43.2%; Pred. No. 1.3e-66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
356 SDTQHSRVLSLYNTINPEASASPCCVSQDLEPLTILYYIGKTPKIEQLSNMIVKSCKCS 414
                                    349 LDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 407
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FILING DATE: 1-SEP-1989
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: 07/790856
FILING DATE: 12-NOV-1991
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: 08/132405
FILING DATE: 12-NOV-1993
                                                                                                                                                           252 GIDGTSTYTSGDQKTIKSTRKKNSGKTPHLLLMLLPSYRLESQQTNRRKKR----- 302
                                                                                                                                                                                                                                                                                 189 PSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSS-------DSKDNTLHVE--
                                                                                                                                                                                                                                                                                                                         135 SAMEKNASN---LVKAEFRVFRLQNPKARVPEQRIELYQILKSKDLTSPTQRYIDSKVVK 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                    289 VPDYASLALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWS 348
                                                                                                                                                                                                    236 -INGFNSGRRGDLATIHGMNR------PFLLLMATPLERAQHLHSSRHRRALDTNSYPYD 288
                                                                                                                                                                                                                                          192 TRAEGEWLSFDVTDAVHEWLHKDRNLGFKISLHCPCCTFVPSNNYIIPNKSEELEARFA 251
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                                                                                                                                                                                                                                                                                                                                                                                                        76 DLLQEKASRRAAACERERSDEEYYAKEVYKIDMPPFFPSENAIPPTFY-RPYFRIVRFDV 134
                                                                                                                                                                                                                                                                                                                                                                                                                                               86 D----RVAGESVEPEPE-PEADYYAKEVTRVLM---VESGNQIYDKFKGTPHSLYMLFNT 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 ALSLSTCSTLDMDQFMRKRIEAIRGQILSKLKLTSPPE--DYPEPEEVPPEVISIYNSTR 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 AAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVP-PGPLPEAVLALYNSTR 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Hasak, Janet E. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 18-MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P0597D1C2D1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
                                                                               -----ALDAAYCFRNVQDNCCLRPLYIDFKRDLGWKWIHEPKGYNANFCAGACPYLWS 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181; Conservative 62; Mismatches 116; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.25 inch, 360 Kb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37.5%; Score 809; DB 1; Length 414; 43.2%; Pred. No. 1.3e-66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFA: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
LENGTH: 414
TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 37.5%; Score 809; DB 5; Length 414; Best Local Similarity 43.2%; Pred. No. 1.3e-66; Matches 181; Conservative 62; Mismatches 116; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Mu-En Lee
APPLICANT: Mark A. Perrella
APPLICANT: Mark A. Perrella
TITLE OF INVENTION: TRANSFORMING GRC
TITLE OF INVENTION: FACTOR- INHIBIT
TITLE OF INVENTION: INDUCIBLE NITRIC
TITLE OF INVENTION: SYNTHASE GENE
TITLE OF INVENTION: TRANSCRIPTION
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Janis K. Fraser
REGISTRATION NUMBER: Reg. No.
REFERENCE/DOCKET NUMBER: 0543
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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                                                                                                                                                                                                                  135 SAMEKNASN---LVKAEFRVFRLQNPKARVPEQRIELYQILKSKDLTSPTQRYIDSKVVK 191
289 VPDYASLALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWS 348
                                           252 GIDGTSTYTSGDQKTIKSTRKKNSGKTPHLLLMLLPSYRLESQQTNRRKKR----- 302
                                                                                  236 -INGFNSGRRGDLATIHGMNR-----PFLLLMATPLERAQHLHSSRHRRALDTNSYPYD 288
                                                                                                                             192 TRAEGEWLSFDVTDAVHEWLHHKDRNLGFKISLHCPCCTFVPSNNYIIPNKSEELEARFA 251
                                                                                                                                                        189 PSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSS------DSKDNTLHVE-- 235
                                                                                                                                                                                                                                                           138 SELREAVPEPVLLSRAELRLLRL---KLKV-EQHVELYQ-----KYSNDSWRYLSNRLLA 188
                                                                                                                                                                                                                                                                                                        76 DLLQEKASRRAAACERERSDEEYYAKEVYKIDMPPFFPSENAIPPTFY-RPYFRIVRFDV 134
                                                                                                                                                                                                                                                                                                                                               86 D----RVAGESVEPEPE-PEADYYAKEVTRVLM---VESGNQIYDKFKGTPHSLYMLFNT 137
                                                                                                                                                                                                                                                                                                                                                                                             18 ALSLSTCSTLDMDQFMRKRIEAIRGQILSKLKLTSPPE--DYPEPEEVPPEVISIYNSTR 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 5 Apri CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      27 AAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVP-PGPLPEAVLALYNSTR 85
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STATE: Massac
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ZIP: 02110-2804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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356 SDTQHSRVLSLYNTINPEASASPCCVSQDLEPLTILYYIGKTPKIEQLSNMIVKSCKCS 414
                                              349 LDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPTVYYVGRKPKVEQLSNMIVRSCKCS 407
                                                                                                        -----ALDAAYCERNVQDNCCLRPLYIDEKRDLGWKWIHEPKGYNANECAGACPYLWS 355
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Search completed: April 15, 2003, 12:01:58 Job time : 27 secs

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Maximum DB seq length: 200000000
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2: /SIDS2/gcgdata/ge
3: /SIDS2/gcgdata/ge
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2159
1 MAPSGLRLLPLLLPLLWLLV......GRKPKVEQLSNMIVRSCKCS 407
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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AAE16943	AAU77101	AAR90827	AAR73596	AAR13813	AAR05258	AAR04034	AAP61468	AAM39186	AAE13596	ID
Human transforming	Human transforming	Pre-transforming g	Human TGF-beta 1 P	Human pro-TGF-beta	Human pre-transfor	Sequence of pre-16	PreTGF-beta gene p	Human polypeptide	Porcine transformi	Description

(USSH) US DEPT HEALTH & HUMAN SERVICES

20-APR-2000; 2000US-199014P. 20-APR-2001; 2001WO-US12980 WO200181404-A2

01-NOV-2001.

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HHNZZOJO	υa	ABB90765	AAU77103	AAW80417	AAR20621	622	AAR73598	AAW78786	AAU77105	AAB08338	ABG20233	ABG20234	ABG06792	AAR12541	AAR53090	AAR79921	AAP91900	AAR05666	AAR05665	AAR05749	AAR20126	AAM40972	AAR29657	AAR27522	AAR05492	AAR05664	AAR05663	AAR03743	AAP81362	AAB84601	AAW78785	AAR83054	AAR46227	AAR20124
	Mutant Transformin	-	transio		rorming	Pig TGF-beta-3. S	Human TGF-beta 3 p	Ω	g transic	O	human	Novel numan diagno	numan	Ω	Polypeptide cross-	Simian-human nybri	Sequence encoded b	Hybrid transformin	Human Transforming	Human TGF-Beta2 ex	Sequence of hybrid	Human polypeptide	TGF-beta 1. Homo	1/be	Chimeric simian TG	Simian Transformin			Human transforming	Nucleotide sequenc	Human pre-transfor	Transforming growt	Human pre-TGF-beta	Sequence of simian

ALIGNMENTS

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RESULT 1
AAE13596
ID AAE1
Porcine; transforming growth factor beta 1; TGF-beta1; gene therapy; IBD; inflammatory bowel disease; autoimmune disease; immunosuppressive; multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus; diabetes mellitus; sarcoidosis; psoriasis; dermatological; mutant;
                                                                                                                                                Ney Location/Qualifiers Misc-difference 223
                                                                                                                                                                                                                                                                                                                                   AAE13596;
                                                                                                                                                                                                                                                                                                                                                         AAE13596 standard; Protein; 390
                                                                                                                                                                                                                mutein.
                                                                                                                                                                                                                                                                                    Porcine transforming growth factor beta 1 (TGF-betal) mutant.
                                                                                                                                                                                                                                                                                                           26-FEB-2002 (first entry)
                                                                                                                               Misc-difference 225
                                                                                                                                                                                       Sus scrofa.
                                                                                                                  /note= "Wild type Cys substituted with Ser"
                                                                                                                                         note= "Wild type Cys substituted with Ser"
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RESULT 2
AAM39186
ID AAM3
XX
AC AAM3
XX
DT 22-0
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         is part of a host suspected of having an autoimmune disease, especially inflammatory bowel disease (IBD), under conditions such that the polypeptide encoded by the nucleic acid sequence in the vector is expressed. The vector is delivered using a delivery system. The delivery of the vector results in substantial elimination of symptoms of the composition is useful for treating various diseases with an autoimmune component such as multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus, insulin-dependent diabetes mellitus, sarcoidosis and psoriasis, and also for assaying the expression of a gene in a cell. The vector is further useful for screening of the effect of test compounds on cytokine (e.g. TGF-beta) expression of transfected cells.
22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tches 390;
                                                                        AAM39186 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a composition containing a vector comprising a gene encoding a regulatory transcription factor under the control of a promoter encoding a transforming growth factor-beta (TGF-beta). The vector is useful for expressing TGF-beta, such as TGF-betal, TGF-beta2 or TGF-beta3, its variants or homologues, by transfecting a cell which
                                         AM39186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is porcine TGF-betal mutant.
                                                                                                                                                                                   344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Composition for treating autoimmune diseases e.g. inflammatory bowel disease in humans, comprises vector containing transforming growth factor-beta under the control of inducible promoter -
                                                                                                                                                                                                                      361
                                                                                                                                                                                                                                                              284
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                                                                                                                                                                      NQHNPGASAAPCCVPQALEPLPIVYYYGRKPKVEQLSNMIVRSCKCS 407
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                                                                                                                                                                                                                                                 YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY 343
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Pred. No. 4.8e-171;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM88642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathles and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activiny, inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for recentor activity cancer diagnosis and therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JAN-2000;
25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          assays for receptor activity, arthritis and inflammation, C.N.S disorders. Note: The sequence data for this patent did not form part \left( \frac{1}{2}\right) = \frac{1}{2}\left( \frac{1}{2}\right) = \frac{1}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang
2hao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 4; SEQ ID NO 2331; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200153312-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peripheral nervous system; neuropathy; central nervous system; CNS;
Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-DEC-2000; 2000WO-US34263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human polypeptide SEQ ID NO 2331.
                           61
                                                                                                                                               1 MPPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
                                                                                                                                                                                             1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
SPPSQGEVPPGPLPEAVLALYNSTRÖRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
                                                                         SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J,
                                                                                                                                                                                                                                                                                                                     366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-442253/47.
DB; AAI58342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acids and polypeptides, useful for treating disorders as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wang Z,
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 390 AA;
                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; 2000US-0620312.
; 2000US-0653450.
; 2000US-0662191.
; 2000US-0693036.
; 2000US-0727344.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                            89.2%; Score 1926.5;
89.9%; Pred. No. 2.46
                                                                                                                                                                                                                                                                                                             10; Mismatches
                                                                                                                                                                                                                                                                                                                                                .4e-160;
                                                                                                                                                                                                                                                                                                                                                                               DB 22; Length 390;
                                                                                                                                                                                                                                                                                                          14;
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. Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yang
                                                                                                                                                                                                                                                                                                      Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             part
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       leukaemias and
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                    В
                                   Ωy
                                                             Matches
                                                                               Query Match
                                                                                                                     The gene product is known to stimulate cell proliferation and inhibit anchorage-dependent growth of a variety of human cancer cell lines, it is esp. useful in treatment of burns and the promotion of surface and internal wound healing. TGF-beta may be expressed from a transformed CHO cell line.
                                                                                                                                                                                                                                                                                                                                                                                EP200341-A
                                                                                                                                                                                                                                                                                                                                                                                                                                  Transforming growth factor beta; cancer; wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PreTGF-beta gene product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAP61468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAP61468 standard; Protein;
                                                                                                                                                                                                      TGF-beta prodn. from transformed hosts - useful esp. wounds (J6 2/9/86).
                                                                                                                                                                                                                                    N-PSDB; AAN60972
                                                                                                                                                                                                                                                                 Derynck
                                                                                                                                                                                                                                                                                                         22-MAR-1985;
13-MAR-1987;
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                                                                                                   Sequence
                                                                                                                                                                                   Disclosure; Fig 1b; 26pp; English.
                                                                                                                                                                                                                                               WPI; 1986-326875/50
                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          284
                                                                     Local Similarity
 61
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                                        \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNSYPYDVPDYASLALDTN 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YLSNRLLAPSDSPEWLSFDVTGVVROWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
                                                             365;
                                                                                                     390 AA;
                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                          85US-0715142.
87US-0025423.
                                                                                                                                                                                                                                                                                                                                          86EP-0302112
                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers 279..390
                                                           88.9%; Score 1919.5; DB 7;
89.7%; Pred. No. 9.9e-160;
tive 10; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   390
                                                               Indels 17;
                                                                                Length 390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      390
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                                                               Gaps
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RESULT 4
AAR04034
ID AAR0
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Query Match
Best Local Similarity
Matches 365; Conserv
                                                                                                                                                                                                                                                                                                                                                                            Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAY-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR04034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR04034 standard; protein; 390
                                                                            Sequence is an exon of transforming growth factor-beta 1 (pre-TGF-beta 1) polypeptide and corresponds to AA's 288-338 of mature TGF-beta 1. The nucleic acid encoding second subtype of TGF-beta (TGF-beta 3) is useful as a probe or to produce TGF-beta 3 for inhibition of normal and
                                                                                                                                                        Nucleotide sequence encoding transforming growth factor beta-3 used as a probe, or to produce TGF beta 3, for inhibiting growth of certain normal and neoplastic cells, eg A549.
                                                                                                                                                                                                        N-PSDB;
                                                                                                                                                                                                                                       Dernyck RM,
                                                                                                                                                                                                                                                                                      08-JUN-1988;
                                                                                                                                                                                                                                                                                                           08-JUN-1988;
                                                                                                                                                                                                                                                                                                                                 14-DEC-1989
                                                                                                                                                                                                                                                                                                                                                        WO8912101-A
                                                                                                                                                                                                                                                                                                                                                                                                             inhibition
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                                             Sequence
                                                                  neoplastic cell growth.
                                                                                                                                     Disclosure; Fig. 2; 61pp; English.
                                                                                                                                                                                                                    WPI; 1990-007474/01.
                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNSYPYDVPDYASLALDTN 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR--------ALDTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRLKKVEQHVELYQKYSNNSWR
                                                                                                                                                                                                       AAQ02815.
                                              390
                                                                                                                                                                                                                                                                                                                                                                                                                                                pre-TGF-beta 1.
                                                                                                                                                                                                                                                                                                                                                                                                                         growth factor beta-3 (TGF beta 3); tumour cells; growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                           Goeddel
                                                                                                                                                                                                                                                                                      88WO-UO01945
                                                                                                                                                                                                                                                                                                             88WO-US01945
                                                                                                                                                                                                                                                                                                                                                                                348..500
                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
             88.9%; Score 1919.5;
89.7%; Pred. No. 9.96
                                                                                                                                                                                                                                           DV;
                .9e-160;
                          DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240
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Conservative

10;

Mismatches

15;

Indels

17; Gaps

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RESULT 5
AAR05258
ID AARC
          N-PSDB;
                       WPI; 1990-051338/07.
                                                                                                                                                                                                                                                                  Cleavage-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGF-potentiated anchorage-independent growth
                                                        Derynck RMA,
                                                                                      (GETH ) GENENTECH INC
                                                                                                                      13-MAR-1987;
                                                                                                                                                     13-MAR-1987;
                                                                                                                                                                                     12-DEC-1989
                                                                                                                                                                                                                      US4886747-A
                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neoplastic cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transforming growth factor-beta-1 (TGF-beta-1);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human pre-transforming growth factor-beta-1 (pre-TGF-beta-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR05258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR05258 standard; protein; 390 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNSYPYDVPDYASLALDTN 300
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          AAQ93301
                                                        Goeddel DV
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                                                                                                                   87US-0025423,
                                                                                                                                                     87US-0U25423
                                                                                                                                                                                                                                                                                                                                                               /note="hydrophobic domain"
82..84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             line inhibition;
                                                                                                                                                                                                                                                                   /note="as above"
277..278
                                                                                                                                                                                                                                                                                                  /note="as above"
176..178
                                                                                                                                                                                                                                                                                                                                  /note="potential N-glycosylation site
136..138
                                                                                                                                                                                                                                                 /note="proteolytic cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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AAR13813
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Best Local
JP03180192-A
                                               Peptide
                                                                            Peptide
                                                                                                            Peptide
                                                                                                                                                            Homo sapiens
                                                                                                                                                                                          Osteogenetic; tumoricidal
                                                                                                                                                                                                                           Human pro-TGF-beta
                                                                                                                                                                                                                                                                                         AAR13813;
                                                                                                                                                                                                                                                                                                                        AAR13813 standard; Protein;
                                                                                                                                                                                                                                                           20-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cleavage of the precursor gives rise to the mature TGF-beta monomer. The sequence for human TGF-beta was determined by direct amino acid sequence analysis and by deduction from the TGF-beta cDNA. It is capable of inducing EGF-potentiated anchorage-independent growth of target cell lines, and/or growth inhibition of neoplastic cell lines. can be used for treating wounds, eg burns or epidermal ulcers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                          344
                                                                                                                                                                                                                                                                                                                                                                                                                                      361
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                                                                                                                                                                                                                                                                                                                                                                                                     NQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YCESSTEKNCCVRQLYIDERKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                              YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                         (first entry)
                                             /note= "pro-TGF-beta
279..390
                                                                            30..390
                                                                                                                          Location/Qualifiers
                                                                                        /note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88.9%;
89.7%;
                              "TGF-beta 1"
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                                                                                                                                                                                                                                                                                                                      390 AA
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X O X K W X E X T X A X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X 
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human pro-TGF-beta 1 prodn., for osteo-genetic activity preparing DNA chain contg. base sequence coding for huma pre:pro-TGF-beta 1, forming expression vector etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Fig 1; 16pp; Japanese.
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N-PSDB; AAQ13392.
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                                                                                                         Transforming growth factor-beta; Human TGF-beta protein; TGF-beta TGF-beta 3; osteogenic cell source; OCS; bone deficiency;
                                                                                                                                                                                           Human TGF-beta 1 protein.
                                                                                                                                                                                                                                                                                                                                                               AAR73596 standard; Protein;
                          Homo sapiens
                                                                            bone-inducing cofactor
                                                                                                                                                                                                                                                   20-DEC-1995
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                                                                                                                                                                                                                                                   (first entry)
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89.7%; Pred. No. 9.9e~160;
tive 10; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                     390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prepro-TGF-beta 1 which it has osteogenetic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 12; Length
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MESULT 8 AAR90827

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AAR90827 standard; Protein;

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Best Local 9
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12-NOV-1991;
18-MAY-1993;
12-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents human transforming growth factor-beta 1 (TGF-beta 1). This sequence and the sequence for human TGF-beta 3 (see ARR73598) are claimed within the scope of the invention. The invention is a composition consisting of a TGF-beta protein and an osteogenic cell source (OCS) formulated in an acceptable carrier other than a bone morphogenic cofactor. This composition can be used for the restoration of bone deficiency. This provides for the generation of mature bone only where it is required, without the inclusion of a specific bone-inducing cofactor. This method can be used with any of the 5 human TGF-beta's or with TGF-beta from other species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Column 15-18; 19pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          carrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Compsn. for treating skeletal tissue deficiency - computransforming growth factor-beta and an osteogenic cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1995-169610/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ammann AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-APR-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                  181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                            121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                    1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
                                                                                                                                                                                                                                            YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
                                                                                                                                                                                                                                                                                                         SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
                                                                                                                                                                                                                                                                                                                         SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
                                                                                                                                                                                                                                                                                                                                                                      MPPSGLRLLPLLLWLLVLTPGPPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA
                                                                        YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY
                                                                                                                      TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR
                                                                                                                                                  SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNSYPYDVPDYASLALDTN 300
                                                                                                                                                                                YLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFT
NOHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS
              NQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 407
                                                         YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY
                                                                                                                                                                                                                                                                                                                                                                                                                                 365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             390 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rudman CG;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89US-0401906.
91US-0790856.
93US-0063841.
93US-0132405.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1919.5; DB 1
Pred. No. 9.9e-160;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                    15; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 390;
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04-AUG-1989;
04-MAR-1992;
05-NOV-1993;
                                                                                                                                                                                  The pre-transforming growth factor (TGF) beta 1 protein is encoded by AAT15720. The mature TGF beta 1 monomer is cleaved from the precursor at the Arg-Arg dipeptide immediately preceding the mature TGF-beta 1 NH2-terminus. It does not contain a recognisable N-terminal signal peptide typical of most secreted proteins. The pre-TGF beta 1 contains several pairs of basic residues which could undergo post-translational cleavage and give rise to separate polypeptide entities. The precursor contains 3 potential N-glycosylation sites, nor of which are localised in the mature TGF beta 1. This is useful in
                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                                                                                      Example 3; Fig 1A-C; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                           New recombinant human
                                                                                                                                                                                                                                                                                                                                                                                                                                           Derynck RMA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-MAR-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US5482851-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cleavage-site
                                                                                                                                                                        purification of the mature protein. TGF beta 1 can be used in, e.g. wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-MAR-1987;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pre-transforming growth factor beta 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-JAN-1980 (first entry)
  61
                                                                                              Local
                                                    1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
                                                                                                                                                                                                                                                                                                                                                                                                                  1996-076891/08.
                          MPPSGLRLLPLLLPLLWLLVLTPGPPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
                                                                                                                                                                                                                                                                                                                                                          ecombinant human transforming growth factor-beta prods. - produce Chinese hamster ovary cells, for use in diagnostic applications
                                                                                                                                                                                                                                                                                                                                                                                                      AAT15720
                                                                                             Similarity
                                                                                                                                    390 AA;
                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              growth factor beta 1; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Goeddel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87US-0025423.
85US-0715142.
89US-0389929.
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93US-0147364
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277..279
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279..39
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176..178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= mature_TGF_beta_1
                                                                                          88.9%;
89.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "potential N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "trypsin-like peptidase cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "potential N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "potential N-glycosylation site"
                                                                                10;
                                                                                           Score 1919.5;
Pred. No. 9.96
                                                                                Mismatches
                                                                                             .9e-160;
                                                                                                        DB 17;
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                                                                               Indels
                                                                                                       Length 390;
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                                                                                                                                                                    Treating a subject with a disorder resulting from insufficient insulin production, and inducing outgrowth of pancreatic cells, involves using a transforming growth factor beta therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; transforming growth factor beta; TGF-beta; insulin production; type I diabetes mellitus; pancreatic cell outgrowth; wound healing; pancreatic duct tissue; ischaemia; stroke; nervous system aging; neurological condition; neurodegenerative disease; inflammation; vasal injury; chemical injury; traumatic injury; tumour-induced injury; amyotrophic lateral sclerosis; spinocerebellar degeneration;
                                                                                                                The invention relates to treating a subject with a disorder resulting
                                                                                                                                          Disclosure; Fig 1; 77pp; English.
                                                                                                                                                                                                                                   WPI; 2002-257468/30
                                                                                                                                                                                                                                                                                                                       09-AUG-2000; 2000US-0635368
                                                                                                                                                                                                                                                                                                                                                    09-FEB-2001; 2001WO-US04192
                                                                                                                                                                                                                                                                                                                                                                                                            WO200212336-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human transforming growth factor beta 1 (TFG-beta-1) polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU77101 standard; Protein; 390
                                                                                                                                                                                                                                                                                           (CURI-) CURIS INC
                                                                                                                                                                                                                                                                                                                                                                                 14-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunological disease; multiple sclerosis; TGF-beta-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR------ALDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFT
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                                                                                                                                                                                                                                                                Pang K;
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from insufficient insulin production, involving contacting the subject with a transforming growth factor beta (TGF-beta) therapeutic. TGF-beta polypeptides can be used for treating a subject with a disorder resulting from insufficient insulin production, e.g. type I diabetes mellitus, and for inducing outgrowth of pancreatic cells associated with pancreatic duct tissue within a subject. A composition comprising a TGF-beta protein may be useful in wound healing and treatment of neurological conditions

derived from acute, subacute or chronic injury to

the nervous

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        including traumatic injury, chemical injury, vasal injury and deficits (such as ischaemia resulting from stroke), together with infectious/inflammatory and tumour-induced injury, aging of the nervous system including Alzheimer's disease, chronic neurodegenerative disease; system including Parkinson's disease, Huntington's chorea, amyotrophic lateral including Parkinson's disease, Huntington's chorea, amyotrophic lateral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sclerosis, spinocerebellar degenerations and chronic immunological diseases of the nervous system or affecting the nervous system, including multiple sclerosis. This sequence represents the human TGF-beta-1
                                                                                                                                                                                                     bone resorption; rheumatoid arthritis; psoriasis; restenosis; atherosclerosis; liver fibrosis; asthma; cytostatic; osteopat
                                                                                                                                                                                                                                    Human; transforming growth factor betal; TGF betal; osteoporosis; latency associated peptide; LAP; Integrin alphavbeta3; apoptosis; immunomodulation; inflammatory disease; fibrotic disease; cancer; diabetic retinopathy; chronic obstructive pulmonary disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                     ophthalmological; antiarteriosclerotic; vasotropic
                                                                                                                                                                                                                                                                                                                          Human transforming growth factor-betal (TGF-betal) protein
                                                                                                                                                                                                                                                                                                                                                              18-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                              AAE16943 standard; Protein; 390
Protein
                                                                                                                                                     Homo
                                  Domain
                                                                Region
                                                                                                  eptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNSYPYDVPDYASLALDTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNNSWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120
                                                                                                                                                     sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY
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365; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            390 AA;
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                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                  Location/Qualifiers
1..29
                                                                                  /label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88.8%;
89.7%;
                                  . 246
                                                "LAP-betal"
                "RGD motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1916.5; DB 23; Length 390;
Pred. No. 1.8e-159;
0; Mismatches 15; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          γ
                                                                                                                                                                        Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of the interaction between latency associated peptide (LAP) of transforming growth factor-betal (TGF-betal) and integrin alphavbeta3. The method is useful for identifying a modulator of the interaction between LAP and integrin alphavbeta3. The method is useful for immunomodulation, in the treatment of inflammatory disease, fibrotic disease, cancer, diabetic retinopathy, bone resorption or osteoporosis, and for preventing apoptosis administering the modulator to the host. The modulator (inhibitor of the interaction between LAP-betal and integrin alphavbeta3) is useful in the manufacture of a medicament for LAP-betal and integrin alphavbeta3 ) is useful in the manufacture of medicament for preventing apoptosis. The modulator is useful in the manufacture of treating a inflammatory or fibrotic disease such as chronic obstructive pulmonary disorder, rheumatoid arthritis, psoriasis, restenosis, liver fibrosis and asthma. The present sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 37-39; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying modulators of interactions between latency associated peptides and integrin alphavbeta3 for therapeutics, by contacting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-097645/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modulates interaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide and integrin with a test product and determining if the product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ludbrook S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GLAX ) GLAXO GROUP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAY-2000;
05-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAY-2001;
   361
                                    284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention relates to a method for identification of a modulator
                                                                                                                                                                                                                                                                                                                                                                                                    MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA
                                                                                                                                                                                                                                                              YDKFKGTPHSLYMLFNTSELREAVPEPYLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR
NQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS
                                                      YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY
                                                                                                                      YLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFT
                                                                                                                                                                                                         YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN
                                                                                                                                                                                                                                                                                                               SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI
                                                                                                                                                                                                                                                                                                                                              SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
                                                                                                                                                                                                                                                                                                                                                                                    MPPSGLRLLLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA
                                      YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY
                                                                                                       TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR--
                                                                                                                                                                                                                                             YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNNSWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGF-betal protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         365;
                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            390 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barry S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000GB-0012991
2001GB-0000286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88.8%; Score 1916.5;
89.7%; Pred. No. 1.8e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Human mature TGF-betal protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Horgan
                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .8e-159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         15; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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AAR20124
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                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                     A new method for treating hypertension comprises administering a furansforming growth factor (TGF)-beta to an individual at a dose effective for lowering blood pressure; the TGF-beta may be e.g. mature TGF-beta, TGF-beta2, a mature TGF-beta1/peta2 hybrid, TGF-beta1 precursor, a latent TGF-beta2 precursor, hybrid TGF-beta1/TGF-beta2 precursor, a latent TGF-beta1 complex or a latent TGF-beta2
                                                                                                                                                                                                                                                                                                                                                                                                                          use of transforming growth factor (TGF)-beta antagonists - for modulating blood pressure, hypertension and hypotension
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-DEC-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1992-024199/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence of
                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                           complex.
                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 1; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BRIM ) BRISTOL-MYERS SQUIB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     «09119513-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypertension therapy; hypotensive agent; blood pressure modulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR20124 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 344 NQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AR20124;
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                                                                                                         61
                                                                                                                                  61
                                                                                                                                                                                                                           Local Similarity
YLSNRLLAPSNSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSKDNTLQVDINGFT
            YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240
                                                                 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
                                                   YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNNSWR
                                                                                                         SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI
                                                                                                                                SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
                                                                                                                                                            MPPSGLRLLPLLLPLLWLLVLTPSRPAAGLSTCKTIDMELVKRKRIETIRGQILSKLRLA
                                                                                                                                                                                     MAPSGLRULPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FB,
                                                                                                                                                                                                                                                                  390 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Comereski CR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   simian transforming growth factor (TGF) beta-1.
                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90US-0541221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein;
                                                                                                                                                                                                                           88.7%;
                                                                                                                                                                                                               10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   390
                                                                                                                                                                                                               Score 1914.5; DB 13;
Pred. No. 2.7e-159;
0; Mismatches 16; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                        for treating
                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                               17;
                                                                                                                                                                                                               Gaps
 240
                                                    180
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RESULT 12
AAR46227
ID AAR46
XX AAR46
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XX AAR46
XX AAR46
XX TGF-
KW TGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-MAR-1985;
13-MAR-1987;
04-AUG-1989;
                                                    cDNA sequences were determined for human pre-TGF-beta-1 (AAQ56923), pig TGF-beta-3 (AAQ56925) and human TGF-beta-3 (AAQ56926), and the corresponding amino acid sequences were determined (AAR46227-29, respectively). A genomic fragment corresponding to a human TGF-beta-1 exon (AAQ56924) was also isolated and its amino acid sequence determined (AAR46239). The sequences have been used in the construction of vectors for the expression of recombinant TGF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human pre-TGF-beta-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR46227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGF-beta-1; TGF-beta-2; transforming growth factor beta-1;
transforming growth factor beta-3; recombinant; wound healing;
                                                                                                                                                                                                                                                                        Disclosure;
                                                                                                                                                                                                                                                                                                                       Nucleic acid sequences encoding transforming growth factor-beta diagnostic probes, and for use in therapeutics
                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Derynk RMA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-MAR-1985;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     344
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YCFSSTEKNCCYRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY
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87US-0025423.
89US-0389929.
92US-0845893.
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82..84
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279..390
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176..178
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136..138
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 Treatment of hypotension, esp. i transforming growth factor-beta
                                                                                                                                                                                               Key
                                                                                                                                                                                                                                                        macrophage inducible nitric oxide synthase; iNOS; constitutive NOS;
interleukin-1-beta; transforming growth factor-beta; TGF-beta; IL1-
                              N-PSDB;
                                                            Lee
                                                                                                 05-APR-1994;
                                                                                                                    05-APR-1994;
                                                                                                                                                          W09526745-A1
                                                                                                                                                                                       Protein
                                                                                                                                                                                                                   Mammalian
                                                                                                                                                                                                                                              nitric oxide production; hypotension; inflammation; septic shock;
                                                                                                                                                                                                                                                                                     Transforming growth factor-beta 1.
                                                                                                                                                                                                                                                                                                                            AAR83054;
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DB; AAT05876.
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                                                                                                                    94WO-US03705
                                                                                                                                                                                     Location/Qualifiers 279..391
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                                                                                                                                                                                                                                                                                                                                                Protein;
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in septic shock - e.g. to inhibit i
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    by administering 
inducible nitric

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RESULT 14
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Best Local S
Matches 365
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                                                                                                                   Key
Domain
                Modified-site
                                                                  Modified-site
                                                                                            Protein
                                                                                                                                                          Homo sapiens
                                                                                                                                                                                  Transforming
                                                                                                                                                                                                         Human pre-transforming growth factor-beta
                                                                                                                                                                                                                                      21-DEC-1998
                                                                                                                                                                                                                                                                                        AAW78785
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                                       Modified-site
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                                                                                                                                                                                  growth
                                                                                                                                                                                                                                    (first entry)
            /note= "Asn is N-glycosylated"
136..138
/note= "Asn is N-glycosylated"
176..178
                                                                                         /note= "hydrophobic domain" 279..390
                                                                 /label= Mat_protein
82..84
  /note=
                                                                                                                                location/Qualifiers
                                                                                                                                                                                                                                                                                         Protein;
                                                                                                                                                                                  factor-beta 1; TGF-beta 1; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88.4%; Score 1909; DB 16;
89.5%; Pred. No. 8.3e-159;
tive 10; Mismatches 15;
"Asn
 is N-glycosylated'
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344 NQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS

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Query Match
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22-MAR-1985;
04-AUG-1989;
04-MAR-1992;
05-NOV-1993;
30-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This is the amino acid sequence of human transforming growth factor-beta 1 precursor (preTGF-beta 1). It was deduced from a preTGF-beta 1 cDNA sequence (see AAN2293). The invention relates to the recombinant production of TGF-beta. Biologically active TGF-beta is defined as being capable of inducing EGF-potentiated anchorage independent growth of target cell lines and/or growth inhibition of neoplastic cell lines. Nucleic acids encoding TGF-beta have been isolated and cloned into vectors which are recovered from transformed cells is used in known therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cleavage-site
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DB; AAV52933.
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                                                                                YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY
                                                                                                                                                                 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR
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                   NQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS
                                                                                                                                             TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR---
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                                                          YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY
                                                                                                                                                                                                                                YLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFT
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3; Fig 1B 1-3; 26pp; English.
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93US-0147364.
95US-0454468.
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85US-0715142.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88.4%; Score 1908.5; DB 19; Length 390; 89.2%; Pred. No. 9.1e-159; tive 10; Mismatches 17; Indels 17;
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to increase yield
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AAB84601
                                                                                  a growth factor, an inhibitor agent, i.e. a protease. The inhibitor agent inhibits the action of at least one specific adverse protein, i.e. a protease, that is upregulated in a damaged tissue such as a wound environment. Growth factors which are included in the composition of the invention are platelet-derived growth factor (PDGF), fibroblast growth factor (FGF), connective tissue derived growth factor (CTGF), keratinocyte-derived growth factor (KGF), transforming growth factor (FGF-beta), granulocyte macrophage colony stimulating factor (GM-CSF), epidermal growth factor (FGF), vascular endothelial growth factor (VGGF), and chrysalin. Inhibitors which are included in the composition of the invention include inhibitors of urckinase type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            platelet-derived growth factor; PDGF; fibroblast growth factor; PGF; connective tissue derived growth factor; CTGF; chrysalin; VEGF; keratinocyte-derived growth factor; KGF, epidermal growth factor; EGF; transforming growth factor-beta; TGF-beta; matrix metalloproteinase; MMP; granulocyte macrophage colony stimulating factor; GM-CSF; uPA; vascular endothelial growth factor; urokinase plasminogen activator;
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                                                                                                                                                                                                                                                                                                                 Composition for the treatment of damaged tissue dermal ulcers comprises an inhibitor agent i.e. factor -
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                          plasminogen activator (uPA) and matrix metalloproteinase (MMP). The composition is useful for the treatment of chronic damaged tissue, wounds and dermal ulcers. The present sequence represents a human TGF-beta, and is used to produce the composition of the invention.
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                                                                                                                                                                                                                                                    The specification describes a pharmaceutical composition, comprising
                                                                                                                                                                                                                                                                                   Disclosure; Page 547; 572pp; English.
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300 283	OY 241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNSYPYDVPDYASLALDTN :
240	QY 181 YLSNRLLAPSDSPEWLSFDVTGVVROWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN
180 180	QY 121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR : :
120 120	Qy 61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEADYYAKEVTRVLMVESGNQI
60	QY 1 MAPSGLRLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIBAIRGQILSKLRLA
Ö	Ouery Match 88.4%; Score 1907.5; DB 22; Length 390; Best Local Similarity 89.2%; Pred. No. 1.1e-158; Matches 363; Conservative 11; Mismatches 16; Indels 17; Gaps

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

TITLE	AUTHORS			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	PIGTGFB1A	RESULT 1
Sporn,M.B. and Roberts,A.B. CDNA cloning of porcine transforming growth factor beta 1 mRNAs.	I (Dases I to 3206) Kondaiah,P., Van Obberghen-Schilling,E., Ludwig,R.L., Dhar,R.,	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Sus scrofa	Sus scrofa (strain miniature swine) cDNA to mRNA.	transforming growth factor-beta-1.	M23703.1 GI:755044	M23703	ca-1 mRNA,	PIGTGFB1A 3206 bp mRNA linear MAM 31-MAR-1995		

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ryakevTrvlwvesGNQ1VbgrKgTpHsLYMLTWITSELREAVPEPVLLSRAELRLLRL
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KLKVEQHVELYQKYSNDSWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTREAIEGFR
LSAHCSCDSKDNTLHVEINGFNSGRRGDLATIHGNNRPFLLLMATPLERAQHLHSSRH
RRALDTNYCFSSTERNGCVRQLYIDFRRCJGWRGYHEPKGYHAMFCLGFCPYIWSLDT
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/strain="miniature swine"
/db_xref="taxon:9823"
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                                        pig.
Sus scrofa
                         Eukaryota;
Mammalia; 1
                                                                   AX338213.1
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JOURNAL Strober, W., Nakamura, K., Kitani, A. and Fuss, Inducible plasmid vector encoding tgf-g(b) patent: WO 0181404-A 1 01-NOV-2001; THE SECRETARY OF THE DEPARTMENT OF HEALTH AN Sequence 1 from AX338213 Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Cetartiodactyla; Suina; Suidae; GI:18128750 1326 bp Patent W00181404 HEALTH AND HUMAN and uses SERVICES Euteleostomi; (SU)

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LSAHSSSDSKDWTLHVEINGFNSGRRGDLATIHGMNRPFILLAATPLEBAQHLHSSRH
RRALDTNVCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDT
QYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS"
4 38 c 392 g 233 t
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RIEAIRGQILsklrlasppsqgdvppgplpeavlalynstrdrvagesvepepepead
YYAKEVTRVLMVESGNQIYDKfKGTPHSLYMLfNTSELREAVPEPVLLSRAELRLLRL
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                                                                                                        (TGF-beta 1)
                                                                                                                                                         Submitted (14-JUL-1988) Jakowlew S.B., National Institute of health, National Cancer Institute, Laboratory of Chemoprevention, Building 41, Room B902, Bethesda, Maryland 20892, USA
                                                                                                                                                                                                                                                                                                                       Porcine mRNA for transforming
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Mammalia;
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                                    porcine
                                     contaminated with porcine cDNA, an porcine TGF-beta-1. 27-MAR-1996
                                                   The submitters believe that the chicken cDNA library was contaminated with porcine cDNA, and that the sequence is
                                                                                      88335639
                                                                                                  Nucleic Acids Res. 16 (17), 8730 (1988)
                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                         Jakowlew, S.B.
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                           Location/Qualifiers
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/translation="MPPSGPGLLPLLLPLLWLIVLTPGRPAAGLSTCKTIDMELVKRK
/translation="MPPSGPGLLPLLPLLWLIVLTPGRPAAGLSTCKTIDMELVKRK
/translation="MPPSGPGLLPLLPLLWLIVNSTRDTVAAGESVEPEPEDAD
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/protein_id="CAA30933.1"
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                                                         Sequence of the porcine transforming Nucleic Acids Res. 15 (7), 3187 (19887174844
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Derynck,R. and Rhee,L.
                                                                                                                                         Sus scrofa
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/organism="Sus scrofa'
/db_xref="taxon:9823"
                                  Location/Qualifiers
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                                                                                                                Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
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                                                                                                       GGCGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTG
                                                                                                                                                  GGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCT
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LSAHCSCDSKDNTLHVEINGFNSGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRH
RRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDT
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RIEAIRGQILSKLRLASPPSQGDvppgplpEavLaLyNsTrDrvagESvEpEPEPEAD
YYAKEVTRVLMLESGNQIYDKFKGTPHSLYMLFNTSELREAVPEPVLLGRAELRLLRL
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/db_xref="GI:2130"
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/clone_lib="lambda gt10"
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                                                                                                                                                               Submitted (20-DEC-2001) Institute of Animal Breeding Science University of Bonn, Endenicher Allee 15, Bonn 53115, Germany
                                                                                                                                                                                           Wimmers, K., Chomdej, S., Direct Submission
                                                                                                                                                                                                                      Polymorphism in the porcine transforming Unpublished 2 (bases 1 to 2221)
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Wimmers, K., Chomdej, S., Ponsuksili, S.
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
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Sus scrofa
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                                                                                                          /organism="Sus scrofa"
/db_xref="taxon:9823"
                           /note="cytokine"
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                                        /gene="TGFB1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L34956.1 GI:516071
homologue; transforming growth factor-beta 1.
Canis familiaris adult jugular vein endothelial cDNA
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Carnivora;
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TEANS ACTION "MPPSGLRLLPLLLPLLPLLVLTPGRPAAGLSTCKTIDMELVKRK RIEAITGGILSKLRUSSPPSGLEVPVVLPEAVLALYNSTRDTVAGESAEPEPEPEAD YYAKEVIRGLMUNENTNIKITSELKRALPLLRL KAKEVIRVLMUNENTNIKITSELKRALPLLRL KLKAEQHVELYKSNDSWRYLSNRLLAPSDTPEMLSFDVTGVVRQWLSHGGEVEGFR LSAHCSCOSKDNTLQVDINGFSSSRRGDLATIHGMNRPFLLMATPLERAGHLHSSRO RRALDTNYCESSTEKNCVQRQL IDFRKDLGRGWWHIEPFKGYHANFCLGCPTYLWSLDT QYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS"
                                                                                                     /product="transforming growth /protein_id="AAA51458.1" /db_xref="GI:516072"
                                                                                                                                                                                                              /gene="TGFB1"
58. .1230
                                                                                                                                                                                                                                                                         /tissue_type="jugular vein endothelial"
/dev_stage="adult"
1. .1369
                                                                                                                                                    /codon_start=1
                                                                                                                                                                   /note="precursor"
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/function="anti-inflammatory
                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9615"
/cell_type="LPS-activated"
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PF 20-MAR-1985 US 85 715142

PR 22-MAR-1985 US 85 715142

PI RIKU MAIKERU ANDORE DERINKU, DEBITSUDO BANNOOMAN GETSUDERU PC C12R1:91), (C12N15/00,C12N15/00,C12R1:91), (C12R1:91);

CC (212N1/00,C12R1:19),(C12N5/00,C12R1:91), (C12N15/00,C12R1:91);

CC strandedness: Double;

CC topology: Linear;

CC hypothetical: No;

CC anti-sense: No;

CC *source: tissue_type=placenta and glyoblastoma; FH Key

Togetfor Consisters
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                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 2527)
  E00973.1 GI:216923
JP 1986219395-A/1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA encoding human TGF-beta
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stem_loop
stem_loop
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                                                                                 mat_peptide
                                                                                                                                       *source: tissue_type=placenta and Location/Qualifiers
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  37. .113
2015. .21
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                                                                                  /product='pre TGF-beta
1676. .2011
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                                                                              TCCTCATGGCCACCCCGCTGGAGAGGGCCCAGCCACCCTGCACAGCTCCCGGCACCCGAG
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888 c 735 g 43
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KLKVEDHYELYQKYSMUSWRYLSMRLLAPSDSPEMLSFDVTGVVRQMLSRGGEIEGFR
LSAHCSCDSRDNTLQVDINGFTTGRRGDLATIHGMNRPELLLMATPLERAQHLQSSRH
RRALDTNYCFSSTEKNCCVRQLYIDFRRDLGWKWIHEPKCYHANFCLGPCPYLWSLDT
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893 c 739 g 432 t
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/db_xref="Gi:412941"
/translation="mPPSGLRLLPLLLPLLWLLVLTPGPPAAGLSTCKTIDMELVKRK
                                                                                                                                                                                                                                                                                                               /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1. .2537
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for preTGF-Betal.
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                GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC
                                                  CTGACGCCTGGCCGGCCGGTCGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG
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GGCAGGCCCGGCCCACCCCCGCCCGCCT-----CACCGGGGCTGTATTTAAGGACA 1317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Woodall,C.J., McLaren,L.J. and Watt,N.J. Sequence and chromosomal localisation of latent transforming growth factor-beta 1 Gene 150 (2), 371-373 (1994)
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Woodall, C.J., McLare
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TGF-beta 1; transforming
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YVAKEVTRVLMVEYGNKIYDKMKSSSHSIYMFFNTSELREAVPEPVLLSRADVRLLRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="SWISS-PROT:P50414"
/translation="MPPSGLRLLPLLLPLLMLTMLTPGRPVAGLSTCKTIDMELVKRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="transforming growth factor-beta
/protein_id="CAA54242.1"
/db_xref="GI:495649"
                                                                                                                                                                                                                                                                                                                                                            LSAHCSCDSKDNTLQVDINGFSSGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRH
RRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDT
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    Woodall, Univ. of Edinburgh, Dept.
of Vet. Studies, Univ. of Edinburgh,

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                                                                                                                       CTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATC 1210
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                                                                                             CTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGTTGTCCAACATGATC
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                                                                                                                                                                                                                                                                                                   GGGCCCTGTCCCTACATCTGGAGCCTGGACACACAGTACAGCAAGGTCCTGGCCCTGTAC
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Query Match Best Local Sin Matches 1142;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parryaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jiff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens, Similar to transforming growth factor, beta MGC:3119 IMAGE:3351664, mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLLL at: http://image.llnl.gov Series: IRAL Plate: 6 Row: e Column: 11 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. CoDNA Sequencing by: Genome Sequence Centre,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (03-NOV-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BC000125.1 GI:12652748
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BC Cancer Agency, Vancouver,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                info@bcgsc.bc.ca
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                                                                                                                                            /translation="mppsglrlllllplumllvltpgrpaaglstcktidmelvkrk riealbegilestektidmelvkrk riealbegilestektidmelvkrk riealbegilestekend riealbegilesteken
                                                                                                   QYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="Similar to transforming growth factor, /protein_id="AAH00125.1" /db_xref="GI:12652749"
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/tlssue_type="Eye, retinoblastor
/clone_lib="NHH_MGC_16"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                          GCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAGGTCCTGGCCC
                                                                              GCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTC
                                                                                                                     TCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCATGCCAACTTCT 1410
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FEATURES

passed the following selection criteria: matched mRNA gi: 37097

clone was selected for full length sequencing because it

source

CDS

/note="Vector: 447 . 1619

/codon_start=1

/lab_host="DH10B-R"

/clone="MGC:2323 IMAGE:3356605" /tissue_type="Eye, retinoblastoma" /clone_lib="NIH_MGC_16"

/organism="Homo sapiens" /db_xref="taxon:9606" Location/Qualifiers Š DЬ Ş В δ 밁 Ş д δÃ Вþ Š

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RESULT 11
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                                                                                                                               Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Matthewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (11-DEC-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 6 Row: e_Column: 10
                                                                                                                                                                                                                                                                                                                                                   cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tissue Procurement: ATCC
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                                                                                                           George Yang, Scott Zuyderduyn, Marco Marra.
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/protein_id="AAH01180.1"
/db_xref="G1:12654683"
/db_xref="G1:12654683"
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RIEAIRGQILSKLRLASPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEEPEAD
YYAKEYTRVLMVETHNEIYDKFKQSTHSIYMFENTSELREAVPEFYLLSRAELRLLRL
YYAKEYTRVLMVETHNEIYDKFKQSTHSIYMFENTSELREAVPEFYLLSRAELRLLRL
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1 648 c 493 g 298 t
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LSAHCSCDSRDNTLOVDINGFTTGRRGDLATIHGMNRPFLLLMATPLERAOHLOSSRH
RRALDTNYCFSSTEKNCCVROLYIDFRKDLGWKWIHEEKGYHANFCLGECPYIWSLDT
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         /translation="MPPSGLRLLPLLLPLLWLLVLTPSRPAAGLSTCKTIDMELVKRK RIETIRGQILSKLKLALSPBSQGEVPPGPLPEAVLALYNGTRDAFDPDEPEAD YYAKEVTRYLAWETHNEIYDKFKQSTHSIVMFFNTSELREAVPEPVLLSRAELLIRL KLKVEQHVELYQKYSNNSWRYLSNRLLAPSNSEEWLSFDVTGVVRQWLSRGGEIEGFR LSAHCSCDSKDNTLQVDINGFTTGRRODLATIHGMNRPELLLMATPLERAGHLQSSRH
                                                                                                                                                  /organism="Cercopithecus
/db_xref="taxon:9534"
262. .1434
RRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDT
                                                                                                                                                                                                          Location/Qualifiers
                                                                                        /protein_id="AAA35369.1"
/db_xref="GI:176553"
                                                                                                                      /codon_start=1
                                                                                                                                 /note="transforming growth
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                                                 CCCTGGATACCAACAGCTACCCATACGACGTGCCAGACTACGCATCTCTGGCCCTGGATA 905
                                                                           TTCTCATGGCCACCCCACTGGAGAGGGCCCAACATCTGCAAAAGCTCCCGGCACCGCCGA- 1095
                                                                                      TCCTCATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCGCACCGCCGAG 845
                                                                                                                                                                             TTAGCGCCCACTGCTCTGTGACAGCAAAGATAACACACTGCAAGTGGACATCAACGGGT
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/product="transforming growth factor-beta"
, 547 c 446 g 267 t
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1096. .1431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QYSKYLALYNQHNPGAṢAAPCCVPQALEPLÞIVYYVGRKÞKVEQLSNMIVRSCKGS"
262. . . 1095
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 971; DB 9;
Pred. No. 5.2e-166;
0; Mismatches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                          GCCCTGGACA 1105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGCAGGCCCGGCCCACCCCCGCCCCCCCCT-----CACCGGGGCTGTATTTAAGGACA 1317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTC
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sig_peptide
FT mat_pep
FT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding human prepro TGF-betal.
                                                      Ohashi,H., Ishii,Y., Miyata,Y., Miyazono,K., Miyagawa,K. and
Takaku,F.
                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1821)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E03028.1 GI:2171250 JP 1991180192-A/1.
                                                                                                                                                                                                                                                                                                                                            PRODUCTION OF HUMAN PRO-TGF-BETAL BY GENETIC RECOMBINATION PAtent: JP 1991180192-A 1 06-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                  KIRIN BREWERY CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                       C12P21/00,C07K13/00,C12N5/10,C12N15/18//C12Q1/68,(C12P21/00C12R1:91),
                                                                                                                                                                                                                                                                        Homo sapiens (human)
JP 1991180192-A/1
06-AUG-1991
07-DEC-1989 JP 1989318243
                                                                                                                                                                                                                                                           OHASHI HIDEYA, ISHII YASUYUKI, MIYATA YOSHINORI,
                                                        CDS
              mat_peptide
                                                                   5'UTR
                                                                                            Key
                                                                                                                                                                           strandedness: Double;
                                                                                                                                                                                                                                   MIYAGAWA KIYOSHI, TAKAKU FUMIMARO
                                                                                                          *source: tissue_type=placenta;
*source: clone=pVC19-TGF;
                                                                                                                                       anti-sense: No;
                                                                                                                                                    hypothetical: No;
                                                                                                                                                                 topology: Linear;
                                                                                                                                                                                          (C12N15/18, C12R1:91);
                            511.
                                            511.
               598. .1680
                            /product='human prepro TGF-beta1' .597
  /note≃′human
                                                                                                Location/Qualifiers
                                                        .1683
 pro TGF-betal
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                                                                       TCCTCATGGCCACCCCGCTGGAGAGGGCCCAGCACCCTGCACAGCTCCCGGCACCCGGCAGGCCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTCTTTACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCGAGCCGGTGTACAACAGCACCGGGAGCCGGGGTGGCCGGGGGAGAGTGCAGAACCGGAGCCCGAGCCCGAGCCCGAGCCCGAGCCCGAGCCCGAGCCCGAGCCGGGTGGCAGAGAGTGCAGAACCGGAGCCCGAGC
                                                                                                                   TCACTACCGGCCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGC
                                                                                                                                                                                          TCAGTGCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGT 725
                                                                                                                                                                                                                                                   ATGTCACCGGAGTTGTGCGGCAGTGGCCTGACCCGCAGAGAGGCCTATAGAGGGTTTTCGCC 665
                                                                                                                                                                                                                                                                                                                                                  GCTCAAGTTAAAAGTGGAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAATCTATGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGG 425
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                                                                                                                                                TCAATTCTGGCCGGGGGGGGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGC
                                                                                                                                                                           TTAGCGCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGT
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679 c 508 g
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84.9%;
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1684. .1820.
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Pred. No. 1.7e-165;
0; Mismatches 143;
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-GCCCTGGACA 1355
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FEATURES

analysis

Location/Qualifiers

Clone distribution: MGC clone distribution information can be found through the I.N.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 27 Row: e Column: 21
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF

source

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REFERENCE
AUTHORS
                                                                                                                                                              COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
BC022242
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                                                 cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94:
                                                                                                                                                                                                          Submitted (01-FEB-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens, clone MGC:22008 IMAGE:4399762, mRNA, BC022242
                                                                                                                                                              NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez,
                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                      Direct Submission
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                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
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                http://www-shgc.stanford.edu (Dickson, Mark) mcd@paxil.stanford.edu
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Primates;
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Catarrhini; Hominidae
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                                                                                                                                                    GCGATACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTG
                                                                                                                                                                                                                                                      GGCTCAAGTTAAAAGTGGAGCAGGACGTGGAGCTATACCAGAAATACAGCAATGATTCCT
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LSAHCSCDSRDNTLQVDINGFTTGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRH
RRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDT
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YYAKEVTRVLMVETHNEIYDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRL
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/protein_id="AAH22242.1"
/db_xref="GI:18490116"
/translation="MFPSGLRLLLLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRK
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/db_xref="taxon:9606"
/clone="MGC:22008 IMAGE:4399762"
/tissue_type="Duodenum, adenocarcinoma"
/clone_lib="NIH_MGC_88"
/lab_host="DH10B"
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84.78;
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Pred. No. 2e-165;
0; Mismatches 147;
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JOURNAL
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-TCGTGCCCCAAGCCCACTTGGGATCGATTAAA 1349
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                                                                                                                                          l (bases 1 to 1560)
Purchlo,A.F., Gentry,L. and Twardzik,D.
Cloning and expression of simian transforming
Patent: EP 0293785-A2 2 07-DEC-1988;
                                                                                                                                                                                          Unclassified
                                                                                                                                                                                                   Unknown
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                                                     Similarity
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                                                                                              /organism="unknown"
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                                                                                                                                Location/Qualifiers
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                                        Score 966.6; DB 6; Pred. No. 3.3e-165; 0; Mismatches 145;
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                                                                                                                                                                                                                                                                     DNA
                                           Indels
                                                              Length 1560;
                                                                                                 others
                                                                                                                                                       growth factor-SS1
                                          60;
                                                                                                                                                                                                                                                                     PAT
                                        Gaps
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AACCAGCACAACCCGGGCGCGTCGGCGCGCGCGTGCTGCCGCAGGCGCTGGAGCCA 11	1091 1290
GGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTCTGTAC 	1031 1230
AAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCATGCCAATTTCTGCCTG	971 1170
ACGGAGAAGAACTGCTGCGTG	911
TACGCATCTCTGGCCCTGGAT	851 1096
ATGGCCACCCGGTTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCCGCGAGCCCTG	791 1041
TCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC	731
GCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT	671 921
ACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCCTCAGT	611 861
TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTC	551 801
AAGTTAAAAGTGGAGCAGGAGCACGTGGAGGCTATACCAGAAATACAGCAATGATTCCTGGCGC 	491 741
CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC	431 681
TATGATAANTTCAAGGGCACCCCCCCACAGCTTATATATGCTGGTTCAACACGTCGGAGCTC	371 621
GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC	311 561
TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG 	251 501
AGCCCCCGAGCCAGGGGACGTGCCGCCCGGCCCGCTGACCTGAGGCAGTACTGGCTCTT	191 441
GTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC 	131 381
CTGACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG	71 321
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Search completed: April 15, 2003, 11:15:38 Job time: 4009 secs

GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

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Perfect score:
Sequence:
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Maximum DB seq length: 200000000
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                         1211.8
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Gapop 10.0 , Gapext 1.0
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| SIDS2/gcgdata/geneseq/geneseqn-emb1/WA1986, DAT: *
| SIDS2/gcgdata/geneseq/geneseqn-emb1/WA1987, DAT: *
| SIDS2/gcgdata/geneseq/geneseqn-emb1/WA1988, DAT: *
| SIDS2/gcgdata/geneseq/geneseqn-emb1/WA1988, DAT: *
| SIDS2/gcgdata/geneseq/geneseqn-emb1/WA1999, DAT: *
| SIDS2/gcgdata/geneseq/geneseqn-emb1/WA1990, DAT: *
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| SIDS2/gcgdata/geneseq/geneseqn-emb1/WA1991, DAT: *
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| SIDS2/gcgdata/geneseq/geneseqn-emb1/WA1994, DAT: *
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AAN60972
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                        AAQ03301
AAQ02814
AAT15720
AAQ56923
AAQ52933
AAQ52933
   AAI58342
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8466.767 Million cell updates/sec
                           Sequence encoding huma sequence of pre-TG pre-TGF-Deta Human pre-TGF-Deta Human pre-transforming simian transformin
                                                                                                                                                                                                                                                                                                                                Description
Human polynucleoti
                                                                                                                                                                                                                                                                  Porcine transformi
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Human transforming	AAT15462	17	339	22.6	307	45	
Transforming Growt	AAQ11993	12	339	22.6	307	44	
	AAA12498	21	3541	22.7	30	43	
Collagen Al/TGF-be	AAT16516	17	3541		30	42	
cDNA encoding the	AAX15245	20	339		30	41	
Human TGF-beta 1 c	AAT17235	17	339		308.6	40	
	AAV99375	20	339		10	39	
TGF-betal active f	AAT42771	18	339	22.8	310.2	38	
ine gen	ABL99528	24	489	26.0	54.	37	
Kidney cancer rela	ABL68818	24	650	26.3	57	36	
Human cDNA dif	ABK84023	24	650	26.3	57.	ა 5	
DNA er	AAS70979	23	875	38.4	22.	34	
Sequence encoding	AAQ12192	12	834	49.9	78.	ω	
DNA encoding novel	AAS84421	23	2773	50.3	84.	32	a
hybr	AAT04115	16	2200	55.5	55.	31	
human	AAN90768	10	2217	56.0		30	
Human TGF-Betal/TG	AAQ05127	11	2207	56.8	773	29	
Hybrid transformin	AAQ03511	11	2207	56.9	774.6	28	
٠,	AAQ03510	11	2206	56.9	774.6	27	
Sequence encoding	AAQ20291	13	2208	57.0	776.2	26	
Human polynucleoti	AAI60128	22	2765	58.6	797.4	25	a
TGF-beta 1. Homo	AAQ29178	13	1565	65.8	896	24	
Human polynucleoti	ABL91703	24	1176	67.3	16	23	
TGF-beta 1/beta 2	AAQ29177	13	1561	68.9	37	22	
Sequence encoding	AAQ04908	11	1561	69.1	40.	21	
	AAQ03509	11	1569	69.6	46.	20	
Coding sequence of	AAN81085	9	1569	69.8	49.	19	
	AAQ03269	11	1571	0	54.	18	
TGFbetal 5'-UTR-CD	AAQ55624	15	4105	0	56.	17	
Monkey transformin	AAQ09317	11	1303	0	57.	16	
Nucleotide sequenc	AAH28216	22	2745	_	65.	15	
cDNA encoding tran	AAT05876	16	2745		65	14	
Simian Transformin	AAQ03508	11	1560		67.	13	
Coding sequence of	AAN81084	9	1560	۳.	O	12	
pro-TGF-	AAQ13392	12	1821	71.1	8	11	
Sequence encoding	AAQ20289	13	1559	71.2	968.6	10	

ALIGNMENTS

RESULT 1 AAD22696

AAD22696 standard; cDNA; 1326 BP

AAD22696;

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Porcine; transforming growth factor beta 1; TGF-beta1; gene therapy; IBD; inflammatory bowel disease; autoimmune disease; immunosuppressive; multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus; diabetes mellitus; sarcoidosis; psoriasis; dermatological; ss.
                                                                                                                                                       CDS
                                                                                 01-NOV-2001.
                                                                                                                                                                                           Sus scrofa
                                                                                                                                                                                                                                                                            Porcine transforming growth factor beta 1 (TGF-betal) cDNA
                                                                                                                                                                                                                                                                                                    26-FEB-2002 (first entry)
                                                                                                          WO200181404-A2.
        (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                  20-APR-2000; 2000US-199014P
                                                         20-APR-2001; 2001WO-US12980
                                                                                                                                                       Location/Qualifiers 16..1188
                                                                                                                               /*tag= a
/product= "Porcine TGF-betal mutant protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a composition containing a vector comprising a CC gene encoding a regulatory transcription factor under the control of a CC promoter encoding a transforming growth factor-beta (TGF-beta). The CC vector is useful for expressing TGF-beta, such as TGF-beta). The CC vector is useful for expressing TGF-beta, such as TGF-betal, TGF-beta (TGF-beta) is part of a host suspected of having an autoimmune disease, especially inflammatory bowel disease (IBD), under conditions such that the CC expressed. The vector is delivered using a delivery system. The delivery of the vector results in substantial elimination of symptoms of the composition is useful for treating various diseases with an autoimmune CC component such as multiple solerosis, rheumatoid arthritis, systemic CC lupus erythematosus, insulin-dependent diabetes mellitus, sarcoidosis and psoriasis, and also for assaying the expression of a gene in a cell. CC compounds on cytokine (e.g. TGF-beta) expression of transfected cells. The present sequence is a cDNA encoding porcine TGF-betal mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Composition for treating autoimmune diseases e.g. inflammatory bowel disease in humans, comprises vector containing transforming growth factor-beta under the control of inducible promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1326 BP; 263 A; 438 C; 392 G; 233 T; 0 other;
541 TTCCTGGCGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTC
                                                                                                              421
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                                                                                                                                   CAACCAAATCTATGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACAC 420
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                                         GCTGAGGCTCAAGTTAAAAGTGGAGCAGCAGCTGGAGCTATACCAGAAATACAGCAATGA 540
                                                                                             GTCGGAGCTCCGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCCT 480
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                            GCTGAGGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGA
                                                                                GTCGGAGCTCCGGGAAGCGGGCGGGAACCTGTATTGCTCTCGGGGCAGAGCTGCGCCT
                                                                                                                                                                                           CGAGCCAGAGGCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGG
                                                                                                                                                                                                                                                                                                                               ACTGGCTCTTTACAACAGTACCCGCGACCGGGGTAGCCGGGGGAAAGTGTCGAACCGGAGCC
                                                                                                                                                                                                                                                                                                                                                          CATGGAGCTGGTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 5.4e-235;
0; Mismatches 7;
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                                                                                                       Sequence encoding preTGF-beta
                                                                                                                                     28-OCT-1991
                                                                                                                                                                                        AAN60972 standard; cDNA;
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CCTGCTCCTCATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGF-beta prodn. from transformed hosts - useful wounds (J6\ 2/9/86).
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13-MAR-1987;
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                                                                                                                                                                                                                                                                                                                                                                                            transformed CHO cell line.
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                                                                                           GGCTCAAGTTAAAAGTGGAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCT 545
                                                       AGCTCCGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGA 485
                                                                                                                                                                 CTCTTTACAACAGTACCCGCGACCCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGC
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                                              AGCTCCGAGAAGCGGTACCTGAACCCGTGTTGCTTCCCGGGCAGAGCTGCGTCTGCTGA
                                                                                 AAATCTATGACAAGTTCAAGCAGAGTACACACAGCATATATGTTCTTCAACACATCAG
                                                                                                                                                        CCCTGTACAACAGCACCCGCGACCGGGTGGCCGGGGAGAGTGCAGAACCGGAGCCCGAGC
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87US-0025423.
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Pred. No. 5e-188;
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               Transforming growth factor-beta-1 (TGF-beta-1); neoplastic cell line inhibition;
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                                                                                         human pre-transforming growth factor-beta-1 (pre-TGF-beta
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                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                 proteins.
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DB; AAR05258.
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CTGAGGCCGACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACG
                     CAGAGGCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACC
                                                    CTCTTTACAACAGTACCCGGGGCCGGGGTAGCCGGGGGAAAGTGTCGAACCGGAGCCCGAGC
                                                                                              TTGCCAGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGG
                                                                                                                                                                                     TAGTGCTGACGCCTGGCCGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCCATCGACATGG 125
                                                                                                                                                                                                                                CCCTGTACAACAGCACCCGCGACCGGGGTGGCCGGGGAGAGTGCAGAACCGGAGCCCGAGC
                                                                                                                                                                                                                      AGCTGGTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGC
                                                                                                                                                                          TGGTGCTGACGCCTGGCCCGCCGGCCGGGACTATCCACCTGCAAGACTATCGACATGG
                                                                                                                                AGCTGGTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                    for therapeutic use
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37..113
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1676..2011
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842..2014
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2015..2100
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84.8%;
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                                                                  GGCAGGCCCGGCCCCACCCCCGCCCGCCT-----CACCGGGGCTGTATTTAAGGACA
                                                                                        TGATCGTGCGCTCCTGCAAGTGCAGCTGAGGTCCCGCCCCGCCCCGCCCCGCCCCGGCAG
                                                                                                    TGATCGTGCGTTCCTGCAAGTGCAGCTGAGGCCCCGCCCCGCCCACAGCCCCGCCCACAC
                                                                                                                                               AGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACA
                                                                                                                                                                                GCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAGGTCCTGGCCC
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CCGTGCCCCAAGCCCACCTGGGGCCCCCATTAA
                                           GCCCGGCCCCACCCCCCCCCCCCCCCCCCCCTGCCTTGCCCCATGGGGGCTGTATTTAAGGACA
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RESULT 4
AAQ02814
ID AAQ02814 standard; cDNA; 2537

ВP

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                                                                                                 Matches 1146;
                                                                                                                       Query Match
                                                                                                                                                                   Sequence encodes the 390 amino acid (AA) precursor transforming growth factor-beta 1 (pre-TGF-beta 1) polypeptide. The 5' untranslated region of the TGF-beta 1 mRNA is 841 bases long, is purine rich and has a region of potential secondary structure. The TATA-like sequence in the 3' untranslated region of the gene is presumably a polyadenylation signal. Mature TGF-beta 1 comprises the C-terminal 112 AA's of pre-TGF-beta 1 and is cleaved at the Arg-Arg dipeptide preceding its NH2 terminus. The nucleic acid encoding the second subtype of TGF-beta (TGF-beta) is useful as a probe or to produce TGF-beta 3 for inhibition of growth of normal and neoplastic cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                        Dernyck RM,
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                                                                                                                                                                                                                                                                                                           Disclosure; Fig. 1b; 61pp; English.
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897
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                                                                                                           Local Similarity
TGGTGCTGACGCCTGGCCCGCCGGCCGGGACTATCCACCTGCAAGACTATCGACATGG
          TAGTGCTGACGCCTGGCCGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCCATCGACATGG 125
                                                 2537 BP; 473 A; 893 C; 739 G; 432 T; 0 other;
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863..911
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37..113
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842..2011
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1677..2011
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                                              GCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTC
                                                                                                                                                 TCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCATGCCAACTTCT
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AGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACA 1205
                                                                                                 GCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAGGTCCTGGCCC
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04-MAR-1992;
05-NOV-1993;
                                       13-MAR-1987;
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25-JAN-1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT15720 standard; cDNA; 2537
                                                                                                                                                                                                     fATA_signal
                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                  nat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                           transforming growth factor beta 1; wound healing;
                                                                                                                                                                                                                       repeat_unit
                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                    recombinant production; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCGTGCCCCAAGCCCACTTGGGATCGATTAAA 1349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGCAGGCCCGGCCCCACCCCCGCCGCCT-----CACCGGGGCTGTATTTAAGGACA 1317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCCCGGCCCACCCCGCCCCCCCCCCCCCCTGCCTTGCCCATGGGGGCTGTATTTAAGGACA 2105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (revised)
(first entry)
87US-0025423.
85US-0715142.
85US-0389929.
89US-0389929.
92US-0845893.
93US-0147364.
                                                         85US-0715142
                                                                                                                                                                                                                                                                                                                                                                           /*tag=
37..113
/*tag=
                                                                                                                                            /*tag= h
2529..2536
                                                                                                                                                                2514..2520
                                                                                                                                                                                                    /*tag= f
2094..2100
                                                                                                                                                                                                                                                                     /product= mature_TGF_beta_1
2015..2100
                                                                                                                /note= "consensus sequence immediately precedes
    polyA-tail (Benoist et al)"
                                                                                                                                                                      /note= "TATA-like sequence;
functions a promote;
                                                                                                                                                                                                                      2019..2023
                                                                                                                                                                                                                                       /note= "GC-rich region; possibly responsible for the
fact 3'UTR of mRNA could not be cloned as cDNA;
                                                                                                                                                                                                                                                                                                 /product= pre-TGF_beta_1
1676..2011
                                                                                                                                                                                                                                                                                                                             842..2014
                                                                                                                                                                                                                                                                                                                                                                                                       1..841
                                                                                                                                                                                             /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                   "GC-rich region forms stable hairpin loops; similar to structural organisation of c-my could play role in mRNA stability or in regulation of transcription"
                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                              may be important for transcription efficiency
                                                                                                                                                                                                                                                                                                                                                                           ۵
                                                                                                                                                                   promoter"
                                                                                                                                                                               that this
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The cDNA encodes the pre-transforming growth factor (TGF) beta 1 protein. The nucleotide sequence was obtd. by an analysis of several overlapping cDNAs and gene fragments. The DNA is useful for the recombinant production of TGF beta 1, which can be used in, e.g. wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New recombinant human transforming growth factor-beta prods. - produc using Chinese hamster ovary cells, for use in diagnostic applications or in therapy
                                                                                                                                                                                                                     486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2537 BP; 473 A; 893 C; 739 G; 432 T; 0 other;
                                                                                                                                                                                                                                                                                                                                             366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC
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Local Similarity 84.8%;
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TTAGCGCCCACTGCTCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGT
                                                                                                                                                                                                                                                                                                                                                                  CTGAGGCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACG 1196
                                                                         ATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGAGGTTTTCGCC
                                                                                                                                                                                                    GGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCT 545
                                                                                                                                                                                                                                                                                                        TCAGTGCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGT
                                                           ATGTCACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGGAAATTGAGGGCTTTCGCC
                                                                                                                       GGCGATACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTG
                                                                                                                                                    GGCGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTG
                                                                                                                                                                                                                                             AGCTCCGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGA
                                                                                                                                                                                                                                                             AGCTCCGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCCTGCTGA 485
                                                                                                                                                                                                                                                                                                                                                                                  CAGAGGCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACC 365
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                                                                                                                                                                                                                                                                                                                               AAATCTATGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGG 425
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                                                                                                                                    TGF-beta-1; TGF-beta-2; transforming growth factor beta-1;
transforming growth factor beta-3; recombinant; wound healing;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             966
                                                                                misc_structure
                                                                                                                             vulnerary; ss.
                                                                                                                                                                Human pre-TGF-beta-1.
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                polyA_signal
                                  mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAGGTCCTGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCCTGGATACCAACAGCTACCCATACGACGTGCCAGACTACGCATCTCTGGCCCTGGATA 905
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                                                                                                                                                                                                                                                                    CCGTGCCCCAAGCCCACCTGGGGCCCCATTAA 2137
                                                                                                                                                                                                                                                                                     TCGTGCCCCAAGCCCACTTGGGATCGATTAAA 1349
                                                                                                                                                                                                                                                                                                       GGCAGGCCCGGCCCACCCCCCCCCCCCCT-----CACCGGGGCTGTATTTAAGGACA 1317
                                                                                                                                                                                                                                                                                                                                            TGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGCGCGTGCCGCAGGCGCTGG
                                                                                                                                                                                                                                                                                                                                                              TGATCGTGCGTTCCTGCAAGTGCAGCTGAGGCCCCGCCCCGCCCACAGCCCCGCCCACCC 1265
                                                                                                                                                                                  (first entry)
                                            /note= "possible h
842..2014
/*tp~-
                /*tag= b
1676..2011
/*tag= c
2515..2521
                                                                                Location/Qualifiers 47..113
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13-MAR-1987;
04-AUG-1989;
04-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA sequences were determined for human pre-TGF-beta-1 (AAQ56923), pig TGF-beta-3 (AAQ56925) and human TGF-beta-3 (AAQ56926), and the corresponding amino acid sequences were determined (AAR46227-29, respectively). A genomic fragment corresponding to a human TGF-beta-1 exon (AAQ56924) was also isolated and its amino acid sequence determined (AAR46230). The sequences have been used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-FEB-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid sequences encoding transforming growth factor-beta diagnostic probes, and for use in therapeutics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2537 BP; 473 A; 890 C; 742 G; 432 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     construction of vectors for the expression of recombinant TGF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 1b; 25pp; English.
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                                                                                                                                                                                                                                                                                                              AGCTGGTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGC
                                                                                                                                                                                                                                                                                                                                       TAGTGCTGACGCCTGGCCGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGG
CTCTTTACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGC
                                                                                                                                                                                                                                                      AGCTGGTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGC
            GGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCT 545
                                                                    AGCTCCGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGA 485
                                                                                              AAATCTATGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGG 425
                                                                                                                                            AGCTCCGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGA
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92US-0845893
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87US-0025423
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84.7%;
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le-187;
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RESULT 7
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                                        Homo sapiens
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                                                                        ransforming growth
                                                                                                           iuman pre-transforming growth factor-beta 1 cDNA
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                                                                                                                                                                                                                                                                                                                              CCGTGCCCCAAGCCCACCTGGGGCCCCATTAA 2137
                                                                                                                                                                                                                                                                                                                                                                TCGTGCCCCAAGCCCACTTGGGATCGATTAAA 1349
                                                                                                                                                                                                                                                                                                                                                                                                     GCCCGGCCCACCCCGCCCCGCCCGCTGCCTTGCCCATGGGGGCTGTATTTAAGGACA
                                                                                                                                                                                                                                                                                                                                                                                                                       GGCAGGCCCGGCCCACCCCCGCCCGCCT-----CACCGGGGCTGTATTTAAGGACA 1317
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                                                                                                                                                     (first entry)
Location/Qualifiers
                                                                        factor-beta
                                                                                                                                                                                                                                  2537
                                                                        1; TGF-beta
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AGCAGGTGAAGCGGAAGCGCATCGAGGCCATCCGCGAGATCCTGTCCAAGCTGCGGC

AGCTGGTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGC

185

956

1016

TGGTGCTGACGCCTGGCCCGGCCCCGGGGACTATCCACCTGCAAGACTATCGACATGG TAGTGCTGACGCCTGGCCGGCCGGCCGCCGGACTGTCCACCTGCAAGACCATCGACATGG 125 Matches 1143; Query Match

Conservative

0;

Mismatches 150; Indels

59;

Gaps

2,

Local Similarity

71.6%; 84.5%;

Score 974; DB 19; Pred. No. 4.6e-187;

Length 2537;

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TGF-beta exon (see AAV52936) restriction fragments as probes.

The 3' region of the sequence was determined using cloned genomic DNA. The invention relates to the recombinant production of TGF-beta. Biologically active TGF-beta is defined as being capable of inducing EGF-potentiated anchorage independent growth of target cell lines and/or growth inhibition of neoplastic cell lines. Nucleic acids encoding TGF-beta have been isolated and cloned into vectors which are replicated in bacteria and expressed in eukaryotic cells. TGF-beta recovered from transformed cells is used in known therapeutic applications. TGF-beta nucleic acids are also useful in diagnosts and expresses acids are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-AUG-1989;
04-MAR-1992;
05-NOV-1993;
30-MAY-1995;
                                                                                                                                                                                          This nucleotide sequence codes for the human transforming growth factor-beta 1 precursor (preTGF-beta 1, see AAW78785). It is a composite of overlapping cDNA clones isolated from different cDNA libraries (placenta, Al72 glioblastoma, HT1080 fibroblastoma) using
Sequence 2537 BP; 475 A; 895 C; 736 G; 431 T; 0 other;
                            also useful in diagnosis and identification of TGF-beta clones.
                                                                                                                                                                                                                                                                                                   DNA encoding transforming growth factor-beta precursor sequence useful for analysis to perform manipulations to increase yield of recombinant production of the protein
                                                                                                                                                                                                                                                                        Example 3; Fig 1B 1-3; 26pp; English.
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22-MAR-1985;
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89US-0389929.

92US-0845893.

93US-0147364.

95US-0454468.
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1676..2011
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/note= "GC-rich sequence"
2514..2520
/*tag= d
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/note= "putative stable hairpin loop"
2015..2100
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                                                                                                                                                        TGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGCGCGTGCTGCGTGCCGCAGGCGCTGG
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 GGCAGGCCCGGCCCACCCCCCCCCCCCCCT-----CACCGGGGCTGTATTTAAGGACA 1317
                                                              TCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCATGCCAACTTCT
                                                                                                                                                                                                                                                                                                                    TCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCATGCCAATTTCT 1025
                                                                                               AGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACA
                                                                                                                            AGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCCAAGGTGGAGCAGCTGTCCCAACA 1205
                                 -----GCCCTGGACA 1685
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Simian transforming growth factor-beta cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-AUG-1990
                                                                                                                                                                                                                                                                                   Inhibition of proliferation of epidermal cells - used to treat psoriasis by contacting cells with compositions containing transforming growth factor-beta.
                                                                                                                                                                                                                                                                                                                                                                                                                  05-AUG-1988;
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                                                                                                                                                                                                       TGF-beta may be used in the treatment of hyperplasia associated with acanthosis-categorised skin diseases, and in alleviating psoriatic symptoms associated with cytokine-induced phenomena. See also AAQ03269 and AAR03750.
                                                                                                                                                                                                                                                                 Disclosure; fig 1; 20pp; English
                                                                                                                                                                                                                                                                                                                                                WPI; 1990-038499/06.
                                                                                                                                                                                                                                                                                                                                                                       Twardzik DR,
                                                                                                                                                                                Sequence 1561 BP; 301 A; 547 C; 446 G; 267 T; 0 other;
                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAR03743
                                                                                                                                                                                                                                                                                                                                                                                           (ONCO-) ONCOGEN LTD PARTNER
 377
                                                                                          257
                                                                                                                                               Local Similarity
                                                                                                     GCCCGGCCCACCCCGCCCGCCCCCGCTGCCTTGCCCATGGGGGCTGTATTTAAGGACA
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                                                                                         TAGTGCTGACGCCTGGCCGGCCGGCCGGCCGACTGTCCACCTGCAAGACCATCGACATGG 125
AGCTGGTGAAGCGGAAGCGCATCGAGACCATCCGCGGCCAGATCCTGTCCAAGCTGCGGC 436
            AGCTGGTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGC 185
                                             TGGTGCTGACGCCTAGCCGGCCGGCCGCAGGACTATCCACCTGCAAGACTATCGACATGG
                                                                                                                                       Conservative
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/*tag= b
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                                                                                                                                                 71.3%;
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                                                                                                                                       0; Mismatches 145;
                                                                                                                                                 Score 971; DB 11;
Pred. No. 1.7e-186;
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                                    TGATCGTGCGCTCCTGCAAATGCAGCTGAGGCCCCGCCCCGCCCCGCCCCACCCCGGCAG
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                                     in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathles and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.
                         specification
                                                                                                                                                                                                                                                                                                                                                                          The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, the immunosuppressant and cytostatic activity. The polynucleotides are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            such as central nervous system injuries
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P-PSDB; AAM39186.
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19-JUL-2000;
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Wang Z,
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Wehrman T,
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Xu C, Xue AJ,
R, Drmanac RT;
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                                                              TCCTCATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCCGCCGAG 845
                                                                                                                                                                                                                                                               TTAGCGCCCACTGCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGT 1556
                                                                                                                                                                                                                                                                                                                 GCGATACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTG
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                           TCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCATGCCAATTTCT 1025
                                                  CCCTGGATACCAACAGCTACCCATACGACGTGCCAGACTACGCATCTCTGGCCCCTGGATA
                                                                                                                                                          TTCTCATGGCCACCCCGCTGGAGAGGGCCCCAGCATCTGCAAAGCTCCCGGCACCGCCGA-
                                                                                                                                                                                                           TCACTACCGGCCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTTCCTGC
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                                                                                                         GCCCTGGACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence encoding simian transforming growth factor (TGF) beta-1.
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                                                                                                                                Use of transforming growth factor (TGF)-beta and their antagonists - for modulating blood pressure, for treating
                                                                                                                                                                                                                                                                                           Oleson FB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mat_peptide
                                                   Disclosure; Fig 1; 42pp; English.
                                                                                                                                                                                                               P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                             20-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-DEC-1991
                                                                                                    hypertension and hypotension
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                                                                                                                                                                                                                                                                                           Comereski CR;
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                                                                                                         ATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCCCCGAGCCCTG
                                                                                                                                                                                                    TCTGGCCGCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTC
                                                                                                                                                                                                                                                                                             GCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT
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                                                                                         ATGGCCACCCCGCTGGAGAGGGCCCCAACATCTGCAAAGCTCCCGGCCACCGCCGA-----
                                                                                                                                                                               ACCGGCCGAGGTGACCTGGCCACAATTCATGGCATGAACCGGCCTTTCCTGCTTCTC
                                                                                                                                                                                                                                                                        GCCCACTGCTCGTGACAGCAAAGATAACACACTGCAAGTGGACATCAACGGGTTCACT
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                                                                                                                                 (KIRI ) KIRIN BREWERY
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pre:pro-TGF-beta 1, forming expression vector etc.
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Local Similarity 84.9%;
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Pred. No. 6.5e-186;
0; Mismatches 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 12; Length 1821;
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       WPI; 1988-347488/49.
P-PSDB; AAP80647.
                                                                                                                                                                                                                                                                         Coding sequence of simian transforming growth factor-beta 1.
                                                                                                                                                                                                                                                                                            09-OCT-1990 (first entry)
                                    Purchio AF,
                                                                         29-MAY-1987;
25-JAN-1988;
                                                                                                     27-MAY-1988;
                                                                                                                        07-DEC-1988
                                                                                                                                          EP293785-A
                                                                                                                                                                   mat_peptide
                                                                                                                                                                                      sig_peptide
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                                                                                                                                                                                                                                                       Transforming
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                                                       (ONCO-) ONCOGEN
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                                                                                                                                                                                                                                                       growth factor-beta 1; tumour treatment; ss cDNA
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88US-0147842
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; ; pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prodn. of simian transforming growth factor beta-1 - by culturing
transfected eucaryotic cells, and new precursor proteins, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence 1560 BP; 301 A; 547 C; 445 G; 267 T; 0 other;
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                                                                                                   GCCCACTGCTCTGTGACAGCAAAGATAACACTGCAAGTGGACATCAACGGGTTCACT
                                                                                                                 GCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT 730
                                                                                                                                                                   ACCGGAGTTGTGCGGCAGTGGCCTGACCCGCAGAGAGGCTTTTGGCGTTTTTCGCCTCAGT 670
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                       ATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGCCCTG
                                                                                                                                                                                                           TACCTCAGCAACCGGCTGCTGGCGCCCAGCAACTCGCCGGAGTGGTTGTCTTTTGATGTC
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Compsns. contg. transforming growth factor beta - used for inhibitions of HTV infection and replication
                                              P-PSDB;
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                                                                                              Brankovan V,
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transforming growth factor-beta e oxide synthase gene transcription
                        Treatment of hypotension, esp. in septic shock - by administering transforming growth factor-beta e.g. to inhibit inducible nitric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     macrophage inducible nitric oxide synthase; iNOS; constitutive NOS; interleukin-1-beta; transforming growth factor-beta; TGF-beta; IL1-nitric oxide production; hypotension; inflammation; septic shock; treatment; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The cDNA encodes transforming growth factor-beta 1 (TGF-beta 1) which has been found to inhibit inducible nitric oxide synthase (iNOS) gene transcription, esp. in interleukin-1-beta (ILI-beta) stimulated rat smooth muscle cells, and at a dose which does not inhibit constitutive NOS. TGF-beta 1 or 2 (AAR83055) or their active fragments, can be used in the treatment of hypotension, such as that associated with severe
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29-DEC-1999;

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The specification describes a pharmaceutical composition, comprising CC a growth factor, an inhibitor agent, i.e. a protease. The inhibitor agent inhibits the action of at least one specific adverse protein, CC i.e. a protease, that is upregulated in a damaged tissue such as a CC wound environment. Growth factors which are included in the composition of the invention are platelet-derived growth factor (PGF), fibroblast CC growth factor (FGF), connective tissue derived growth factor (CTGF), CC keratinocyte-derived growth factor (KGF), transforming growth factor (GM-CSF), epidermal growth factor (KGF), transforming growth factor (GM-CSF), and chrysalin. Inhibitors which are included in the CC composition of the invention include inhibitors of urokinase-type plasminogen activator (UPA) and matrix metalloproteinase (MMP). The CC composition is useful for the treatment of chronic damaged tissue, i.e. wounds and dermal ulcers. The present sequence encodes a human TGF-beta, and is used to produce the composition of the invention.
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Pred. No. 2.1e-185;
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                                                            CAGGCCCGGCCCACCCCGCCCGCCCCCCCTGCCTTGCCCATGGGGGGCTGTATTTAAGG
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US-07-669-171-1
                                                                                                                  Sequence 1, Application US/07669171 Patent No. 5304541 GENERAL INFORMATION:
            APPLICANT: PURCHIO, ANTHONY F.
APPLICANT: MADISEN, LINDA
APPLICANT: MERWIN, JUNE RAE
TITLE OF INVENTION: TGF-b1/b2: A NOVEL CHIMERIC TRANSFORMING
TITLE OF INVENTION: GROWTH FACTOR-BETA
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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LOCATION:
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TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1560 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity Matches 1146; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 56
TELECOMMUNICATION IMPORMATION:
TELEPHONE: 212-790-9090
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/0 FILING DATE: 19910314 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
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AAGTTAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC
                                                            CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC
                                                                                                                         TATGACAAGTTCAAGCAGAGCACACAGCATATATATGTTCTTCAACACATCAGAGCTC
                                                                                                                                            TACAACAGCACCCGCGACCGGGTGGCCGGGGAGAGTGCGGAGCCGGAGCCCGAACCGGAG
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                                       CGAGAAGCAGTACCTGAACCTGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGAGGCTC
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Pred. No. 8e-197;
0; Mismatches 142;
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        Sequence 28, Application US/09661753

Patent No. 643699

Patent No. 643699

PATENT: NISONASTION:

APPLICANT: NISONAS M. Dean
APPLICANT: Susan F. MULICAY

APPLICANT: SUSAN F. MOLICAY

APPLICANT: SUSAN F. MOLICAY

APPLICANT SUSAN F. MOLICAY

APPLICANT SUSAN F. MOLICAY

FILE REFERENCE: ISPH 0498

CURRENT APPLICATION NUMBER: US/09/661,753

CURRENT FILING DATE: 2000-09-14

EARLIER APPLICATION NUMBER: 05/154,546

EARLIER FILING DATE: 1999-09-17

NUMBER OF SEQ ID NOS: 68
SEQ ID NO 28
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (842)...(2017)
US-09-661-753-28
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Best Local
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Pred. No. 9.9e-196;
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RESULT 4
PCT-US94-03705-3
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application PC/TUS9403705 GENERAL INFORMATION:
                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Janis K. Fraser
                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Mark A. Perrella

TITLE OF INVENTION: TRANSFORMING GROWTH

TITLE OF INVENTION: FACTOR INTERITS

TITLE OF INVENTION: INDUCTBLE NITRIC OXIDE

TITLE OF INVENTION: SYNTHASE GENE

TITLE OF INVENTION: TRANSCRIPTION
                                                                                                                                                                                                                                                                    SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2046
                                                                         REGISTRATION NUMBER: Reg. No. 34,819
REFERENCE/DOCKET NUMBER: 05433/007001
ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
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                                                TELEFAX:
                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 5 Apr. CLASSIFICATION:
                                                                  TELEPHONE:
                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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225 Franklin Street
                                               : (617) 542-5070
(617) 542-8906
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TOPOLOGY: line
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Local Similarity 84.6%;
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                                                                           GAGCCCTGGATACCAACAGCTACCCATACGACGTGCCAGACTACGCATCTCTGGCCCTGG
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                                                                                                                                                                                                                                                                                                                                                                                   -GAGGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATT
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מט		US-07-669-171-3
. Y		GY: linear
		NUCLEIC ACID
ط ا		CHARACTERISTICS:
Оу		; INFORMATION FOR SEQ ID NO: 3:
ממ		X: 21
Оy	,	CATION INFORMATION: 212-790-9090
ממ	24-159-999	TRATION NUMBER: 18,872
Qy		; ATTORNEY/AGENT INFORMATION: ; NAME: MISROCK, S. LESLIE
Db		; FILING DATE: 19910314 ; CLASSIFICATION: 435
Qy	,171	; CURRENT APPLICATION DATA: ; APPLICATION NUMBER: US/07/669,171
Db	#1.0, Version #1.25	In Release #
Ϋ́		IBM PC compatible
		EADABI
ı Qy		COUNTRY: U.S.A.
)		
Db	AMERICAS	E: PENNIE & EDMONDS
Qy		••• (
DЬ		VENTION: GROWTH
Qy	A NOVEL CHIMERIC TRANSFORMING	JUNE RAI
рь		; APPLICANT: PURCHIO, ANTHONY F. ; APPLICANT: MADISEN, LINDA
QΥ		O. 5304541 INFORMATION:
Db		US-07-669-171-3 ; Sequence 3, Application US/07669171
Qy		RESULT 5
da	CCCATTAA 2140	Ĝ.
Qу	CGATTAAA 1349	QY 1315 ACATCGTGCCCCAAGCCCACTTGGGATCGATTAAA
Db	CAGGCCCGGCCCACCCCGCCCCGCCCCGCTGCCTTGCCCATGGGGGGCTGTATTTAAGG 2105	Db 2046 CAGGCCCGGCCCACCCGCCGCCGCC
Qy	CGCCTCACCGGGCTGTATTTAAGG 1314	QY 1263 CCCGGCAGGCCCGGCCCACCCCCGCCCGCCCGCCT-
Дb	ACATGATCGTGCGCTCCTGCAAGTGCAGCTGAGGTCCCGGCCCGGCCCCGCCCCGCCCCGG 2045	Db 1986 ACATGATCGTGCGCTCCTGCAAGTGCAGCTGAGG
Qy		QY 1203 ACATGATCGTGCGTTCCTGCAAGTGC
Db		1926
Qy	TGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCA 1202	Qy 1143 TGGAGCCACTGCCCATCGTGTACTAC
dd		1866
0v	CTCTGTACAACCAGCACAACCCGGGCGCGCGCGCGCGCGC	Qy 1083 CTCTGTACAACCAGCACAACCCGGGC
Db		Db 1806 TCTGCCTCGGGCCCTGCCCTACATTTGGAGCCT
Qy	TCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGG 1082	Qy 1023 TCTGCCTGGGGGCCCTGTCCCTACATO
Z W (C	ACTIVCGGAAGGACCIGGGCIGGAAGIGGAIICAIGACCCAAGGGCIACCAIGCCAAIG CCAII 	QY 953 ACTICCGGAAGGACCTGGGCTGGAAGTGGAT
		

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Query Match 67.8
Best Local Similarity 83.2
Matches 1124; Conservative
                                                                                                                               1104 -----
1176 AAGAGGGATCTAGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCATGCCAACTTCTGC
             968 CGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCATGCCAATTTCTGC 1027
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Pred. No. 1.2e-186;
0; Mismatches 164;
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CURRENT APPLICATION UNMBER: US/09/661,753
CURRENT FILING DATE: 2000-09-14
EARLIER APPLICATION NUMBER: 60/154,546
EARLIER FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 68
SEQ ID NO 1
LENGTH: 2094
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
LOCATION: (868)...(2040)
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APPLICANT: NICHOLAS M. Dean
APPLICANT: SUSAN F. MULTAY
TITLE OF INVENTION: ANTISENSE MODULATION OF
FILE REFERENCE: ISPH-0498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application Patent No. 6436909
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RESULT 7
US-09-661-753-27
; Sequence 27, Application
; Patent No. 6436909
; GENERAL INFORMATION:

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EARLIER APPLICATION NUMBER: 60/154,546
EARLIER FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 68
SEQ ID NO 27
LENGTH: 1585
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APPLICANT: Susan F. Murray
TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA
FILE REFERENCE: ISPH-0498
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                                                                                                                                                                                                                                                                                                                                                                                          CCGAGGCGGACTACTACGCCAAAGAAGTCACCCGCGTGCTAATGGTGGACCGCAACAACG
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                                                                                                                                                                                                                                                          GATTCAAGTCAACTGTGGAGCAACACGTAGAACTCTACCAGAAATATAGCAACAATTCCT
                                                                                                                                                                                                                                                                          GGCTCAAGTTAAAAGTGGAGCAGGAGCAGGGGGGGTATACCAGAAATACAGCAATGATTCCT
                                                                                                                                                                                                                                                                                                                         AGCTCCGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGA 485
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TCAGTCCCAAACGTCGAGGTGACCTGGGCACCATCCATGACCTGACCCATCCTGC 1187
                                TCAATTCTGGCCGCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGC 785
                                                              TCAGTGCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGT 725
                                                                                                                             ACGTCACTGGAGTTGTCCGGCAGTGGCTGAACCAAGGAGGACGGAATACAGGGCTTTCGCT
                                                                                                                                                           ATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCC 665
                                                                                                                                                                                             GGCGTTACCTTGGTAACCGGCTGCTGACCCCCACTGATACGCCTGAGTGGCTGTCTTTTG
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Pred. No. 1.7e-166;
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RESULT 8
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NUMBER OF SEQUENCES: 16
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Patent No.
                                                                                                                                                                                                                                                                  SEQ ID NO:3:
                                                                                                                                                                                                        Query Match
                                                                                                                                                                            Matches 963;
                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/07/446,020 FILING DATE: 05-DEC-1989 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: CLONING AND EXPRESSION OF TRANSFORMING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: PURCHIO, ANTHONY F.; MADISEN, LINDA; WEBB, NANCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              966 TCCGGAAGGACCTGGGCTGGAAGTGGAATTCATGAACCCAAGGGCTACCATGCCAATTTCT 1025
                                                         316
                                                                                                                 APPLICATION NUMBER: 148,267
FILING DATE: 25-JAN-1988
APPLICATION NUMBER: 106,752
FILING DATE: 06-OCT-1987
                                                                                                                                                                                                                                                                                                                                         FILING DATE: 16-DEC-1988
APPLICATION NUMBER: 234,065
FILING DATE: 18-AUG-1988
                                                                       LENGTH: 2207
                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 285,140
                                                                                                                                                                                          Match 56.8%;
Local Similarity 78.4%;
                                                                                                                                               CCCTGGATACCAACAGCTACCCATACGACGTGCCAGACTACGCATCTCTGGCCCCTGGATA 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGATCGTGCGCTCCTGCAAGTGCAGCTGA 1585
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                                                         TGGTGCTGACGCCTAGCCGGCCGGCCGCAGGACTATCCACCTGCAAGACTATCGACATGG
 AGCTGGTGAAGCGGAAGCGCATCGAGACCATCCGCGGCCAGATCCTGTCCAAGCTGCGGC
                          AGCTGGTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGC
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                                                                                                                                                                            Conservative
                                                                                                                                                                          Score 773; DB 6; 1
Pred. No. 5.6e-155;
0; Mismatches 215;
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                                                                                     AACCTCTAACCATTCTCTACTACATTGGCAAAACACCCAAGATTGAACAGCTTTCTAATA
                                                                                                                                  AGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACA 1205
                                                                                                                                                                          TATATAATACCATAAATCCAGAAGCATCTGCTTCTCCTTGCTGCGTGTCCCAAGATTTAG
                                                                                                                                                                                                                            GTGCTGGAGCATGCCCGTATTTATGGAGTTCAGACACTCAGCACAGCAGGGTCCTGAGCT 1284
                                                                                                                                                                                                                                                                                            GCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTC 1085
                                                                                                                                                                                                                                                                                                                                                              TCAAGAGGGATCTAGGGTGGAAATGGATACACGAACCCAAAGGGTACAATGCCAACTTCT
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US-08-470-837-29
                                                                                                                                                                                                                                   Query Match
---+ rocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2
Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 310-445-9031 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/470,837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Cheung, David T.
TITLE OF INVENTION: Transfo
TITLE OF INVENTION: and
TITLE OF INVENTION: Their U
                1076 GTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGGCGCCGTGCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION: NAME: Sharp, Janice A.
                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 339 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                          956 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 1015
                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 11150 Sant
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                               LOCATION:
                                                                                                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                           LOCATION:
                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 34,051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 90025-3395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                             GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG
                                                                                                                                                                        GCCAACTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG
                                                                                                         TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCATGAGCCCAAGGGCTACCAT 120
29, Application US/08470837
o. 5800811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
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11150 Santa Monica J
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                                                                                                                                                                                                                                   Conservative
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Hall, Frederick L.
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94.7%;
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Their Use in Wound Healing
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                                                                                                                                                                                                                                               Score 310.2; DB 1;
Pred. No. 2.9e-57;
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                                                                                                                                                                                                                                   Mismatches
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RESULT 10
US-08-486-057B-1
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; LOCATION: US-08-486-057B-1
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                                                                                                                                                                                                                                                     TELEFAX: (908) 277-43 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 339 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Process for Refolding Recombina TITLE OF INVENTION: Produced TGF-beta-like Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cerletti, Nico
APPLICANT: McMaster, Gary K.
APPLICANT: Cox, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1196 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1234
                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: GB 8927546.5
FILING DATE: 06-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5650494ak, Henry P.
REGISTRATION NUMBER: 33200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/201,703 FILING DATE: 25-FEB-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Rel
                                                          FEATURE:
                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
FILING DATE: 03-DEC-1990
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Schmitz, Albert APPLICANT: Meyhack, Bernd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1136 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 1195
                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                          NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 520 Whi
CITY: Tarrytown
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A. ZIP: 10591-9005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 0' FILING DATE: 13-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                      NAME/KEY:
                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 4-17861/+/Cont3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/0 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Henry P. No. 5650494ak
520 White Plains Road, P.O. Box 2005
                                                                                                                                                                                                                                                                     (908)
                                      CDS
                                                                                            CDS
              1..339
                                                                                                                                                      linear
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                                                                                                                                DNA (genomic)
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RESULT 11
US-08-789-588-1
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Best Local Similarity
Matches 320; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cerletti, N:
APPLICANT: McMaster, G
APPLICANT: Cox, David
APPLICANT: Schmitz, All
APPLICANT: Meyhack, Bei
                                                                                                                 APPLICATION NUMBER: US 08/486,057
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/201,703
FILING DATE: 25-FEB-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 0: FILING DATE: 13-OCT-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES:
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                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                    CLASSIFICATION: 530 PRIOR APPLICATION DATA:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 120
                                   FILING DATE:
APPLICATION NUMBER:
                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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Y: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                520 White Plains Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Meyhack, Bernd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cerletti, Nico
                                                                                                                                                                                                                                                                                         PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schmitz, Albert
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                                   03-DEC-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gary K.
   GB 8927546.5
                                                   US 07/621,502
                                                                                                    US 07/960,309
                                                                                                                                                                                                                                                         US/08/789,588
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Pred. No. 6.4e-57;
0; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                P.O. Box 2005
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TTORNEY/AGENT INFORMATION:

NAME: No. 5922846ak, Henry REGISTRATION NUMBER: 33200

5922846ak, Henry

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4-17861/+/Cont3

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Best Local S
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Patent No. 6057430
GENERAL INFORMATION:
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                             CLASSIFICATION: 530
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                           COMPUTER READABLE FORM:
COMPUTER READABLE Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                        TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                           1076
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 4-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
                                                                                                                                                                                                                                                                                                                                         1196
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LOCATION:
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LOCATION:
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STRANDEDNESS: double
TOPOLOGY: linear
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         TYPE: r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
mes 320; Conserv
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                                                                        FILING DATE:
                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                              CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT
                                                                                                                                                                                                                                                                                                                                                                 CAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCCAAGGTGGAGCAG
                                                                                                                                                                                                                                                                                                                                                                                          CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCCAAGGTGGAGCAG
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         : 339 base
nucleic aci
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Je pairs
Racid
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                                                                                                                                                                                  No. 6057430el process for the production biologically active dimeric protein
                                                                                   US/09/123,233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 308.6; DB 2;
Pred. No. 6.4e-57;
0; Mismatches 19;
                                                                                                            Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 339;
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; LENGTH: 337
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(336)
US-08-868-452-29
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Sequence 20, Appr
Sequence 20,
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Best Local Similarity
Matches 320; Conserv
Query Match
Best Local Similarity 94.7
Matches 319; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 29
                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/08/868,452C
CURRENT FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: BONE MORPHOGENETIC PROTEINS TITLE OF INVENTION: USE IN BONE GROWTH FILE REFERENCE: 1972-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bo Han APPLICANT: Edwin Shors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Marcel E. Nimni
APPLICANT: Frederick L. Hall
APPLICANT: Lingtao Wu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: CI
HYPOTHETICAL: NO
IMMEDIATE SOURCE:
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LOCATION: 1..336
OTHER INFORMATION:
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                                          Score 308.2; DB 4; Pred. No. 7.7e-57;
       Mismatches
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RESULT 14
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; APPLICANT: DERYNCK, RIK M.A.;GOEDDEL, DAVID V.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING TGF-B
; NUMBER OF SEQUENCES: 21
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APPLICATION NUMBER: US/07/389,929
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                                             AAAACGAAACCAACCTGTTCCGGGCAGAATTCCGGGTCTTGCGGATGCCCAACCCCAGCT 742
                                                                                    TGCCGGAACCTGTATTGCTCTCCGGGCAGAGCTGCGCCTGCTGAGGCTCA------
                                                                                                                          CCGTTTGCCCCAAAGGAATCACCTCCAAGATTTTCCGCTTCAACGTGTCGTCAGTGGAGA 682
                                                                                                                                                                   TCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTCCGGGAAGCGG 440
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                                                                                                                                                                                                                                                                               Sequence 1, Application PC/TUS9104541
GENERAL INFORMATION:
APPLICANT: Oncogene Science Inc.
TITLE OF INVENTION: TISSUE DERIVED TUMOR GROWTH INHIBITORS
NUMBER OF SEQUENCES: 2
                 ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               803 CCAAGCAGCGCTACATCGACGGCAAGAACCTGCCCACGCGGGGTGCCGCCGAGTGGCTGT
APPLICATION NUMBER:
                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                   CITY: New York
STATE: New York
                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGT 1199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCTGGAGCCCCTGACCATCCTGTACTACGTCGGGAGGACCGCCAAGGTGGAGCAGCTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCATGCCA 1019
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                                                                                                                                                                                                                            30 Rockefeller Plaza
                                                                                                                                                                 USA
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LOCATION: 263..1498
COTHER INFORMATION:
PCT-US91-04541-1
                                        QΥ
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ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1919,
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
TELEPHONE: (212)977-9550
TELEPHONE: (212)64-0525
TELEEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2529 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECILE TYPE: COMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Querly Match 18.1%; Score 245.8; DB 5; Length 2529; Best Local Similarity 53.3%; Pred. No. 1.7e-43; Matches 666; Conservative 0; Mismatches 532; Indels 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: N
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Transforming Growth Factor-Beta
IMMEDIATE SOURCE:
CLONE: TGF-B3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EATURE:
                                            390 TTAGGGGACAGATCTTGAGCAAGCTCAGCCTCACCAGCCCCCTGAGCCAACGGTGATGA 449
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744 CTAAGCGGAATGAGCAGAGCATCGAGCTCTTCCAGATCCTTCGGCCAGATGAGCACATTG
                                                                                         684 AAAATAGAACCAACCTATTCCGAGCAGAATTCCGGGTCTTGCGGGTGCCCAACCCCAGCT 743
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                                                                                                                                                                                                                                                                                                      321 ACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATCTATGATAAAT 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          450 CCCACG-----TCCCCTATCAGGTCCTGGCCCTTTACAACAGCACCCGGGAGCTGCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  270 TGCACTTGCAAAGGGCTCTGGTGGTCCTGGCCCTGCTGAACTTTGCCACGGTCAGCCTCT 329
                                                                                                                                                                                                                                                                                                                                                                   504 AGGAGATGCATGGGGAGGGAGGGAAGGCTGCACCCAGGAAAACACCGAGTCGGAATACT
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LOCATION: 263..1498
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96 GACTGTCCACCTGCAAGACCATCGACATGGAGCTGGTGAAGCGGAAGCGCATCGAGGCCA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 receeracrecrecrecrecrecrecracrecracrecreaceccreeceeceecee 95
                                                                                                                                      TGCCGGAACCTGTATTGCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTCAAGTTAAAAG 500
                                                                                                                                                                                  CTGTCTGCCCTAAAGGAATTACCTCCAAGGTTTTCCGCTTCAATGTGTCCTCAGTGGAGA 683
                                                                                                                                                                                                          TCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTCCGGGAAGCGG 440
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1194 AGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGAGGCCCCGC
1134 CGCAGGCGCTGGAGCCACTGCCCATCGTGTACCTACGTGGGCCGCAAGCCCAAGGTGGAGC
1074 AGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGGCGCGTGCTGCGTGCG
1014 ATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCA
954 TCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACC
894 TGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGGCGCAGC
834 GGCACCGCCGAGCCCTGGATACCAACAGCTACCCATACGACGTGCCAGACTACGCATCTC
774 GGCCCTTCCTGCTCCTCATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCC
AAATTAACGGGTTCAATTCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACC
TTCGCCTCAGTGCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGG
CCTTTGATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTT
ATTCCTGGCGCTACCTCAGCAACCGGCTGCTGCTGCCCCAGTGACTCACCGGAGTGGCTGT

Search completed: April 15, 2003, 11:53:59 Job time: 112 secs

563

803

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Database :
                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OM nucleic - nucleic search, using sw model
       US-10-017-372E-36
1361
1 tggtaccgagatggcgcctt.....cgattaaagcggccgcgact 1361
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Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    593429 seqs, 438583890 residues
                                                                                                                                                                                                                                                                                                                       Published_Applications_NA: *
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                  /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
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/cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
                                                                                                                                                                             /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. 2 2 3 4 5 5 6 6 6 8 8 9 10	Score 965.8 965.8 847 847 827.4 6591.4 591.4 591.6 308.6 227.2 209.4 182.4	Query Match 	Query Match Length	DB 10 10 10 10 10 10	US-09-948-002-28 US-09-948-002-21 US-09-948-002-27 US-09-756-283A-19 US-09-756-283A-21 US-09-813-271B-1 US-09-813-271B-7 US-09-813-271B-5 US-09-813-271B-1 US-09-813-271B-1	Description Sequence 28 Sequence 1, Sequence 27 Sequence 2 Sequence 2 Sequence 1 Sequence 2 Sequence 2 Sequence 2 Sequence 3 Sequence 5 Sequence 5 Sequence 5
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4	654	48.1	1376	10	US-09-756-283A-19	Seq
υ	591.4	43.5	1352	10	US-09-756-283A-21	Seq
6	308.6	22.7	339	10	US-09-813-271B-1	Seq
7	245.8	18.1	2574	12	US-10-028-158-20	Seq
80	227.2	16.7	336	10	US-09-813-271B-7	Seq
9	209.4	15.4	339	10	US-09-813-271B-5	Sequ
10	182.4	13.4	336	10	US-09-813-271B-11	Segi
11	180.8	13.3	336	10	US-09-813-271B-9	Sequ
12	179.8	13.2	4267	9	US-09-948-002-47	Sequence
13	158.2	11.6	339	10	US-09-813-271B-3	Sequence
14	158.2	11.6	2912	12	US-10-044-090-323	Sequence
	141.6	10.4	597	10	US-09-864-761-15319	Sequence
c 16	134.8	9.9	154	10	US-09-864-761-31841	Sequence
c 17	131.8	9.7	206	10	US-09-833-381-577	Sequence
c 18	122	9.0	537	10	US-09-864-761-8844	Sequence
19	121	8.9	148	10	115-00-961-761-35510	Sequence

ALIGNMENTS

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; LOCATION: (842)...(2017)
US-09-948-002-28
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; Sequence 28, Application US/09948002
; Publication No. US20030050265A1
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                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 1146; Conserv
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SEQ ID NO 28
LENGTH: 2745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Nicholas M. Dean
APPLICANT: Susan F. Murray
TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
TITLE OF INVENTION: FACTOR BETA EXPRESSION
FILE REFERENCE: ISPH-0607
CURRENT APPLICATION NUMBER: US/09/948,002
CURRENT FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: 09/661,753
PRIOR APPLICATION NUMBER: 60/154,546
PRIOR APPLICATION NUMBER: 60/154,546
PRIOR FILING DATE: 1999-09-17
PRIOR FILING DATE: 1999-09-17
                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
    957
                                                                            126 AGCTGGTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGC 185
                                                                                                                                                             837 CCCCCATGCCGCCCTCCGGGCTGCGGCTGCTGCTGCTGCTGCTACCGCTGCTGTGGCTAC 896
                                                                                                                                                                                                      AGCTGGTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGC 1016
                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                          71.0%; Score 965.8; DB 9;
84.6%; Pred. No. 1.8e-251;
tive 0; Mismatches 147;
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LENGTH: 2094
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APPLICANT: Susan F. Murray
TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
TITLE OF INVENTION: FACTOR BETA EXPRESSION
FILE REFERENCE: ISPH-0607
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CURRENT FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: 09/661,753
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LOCATION: (868)...(2040)
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80.8%;
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Pred. No. 2.2e-219;
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APPLICANT: NICHOIAS M. Dean
APPLICANT: SUSAN F. MUTTAY
TITLE OF INVENTION: FACTOR BETA EXPRESSION
FILE OF INVENTION: FACTOR BETA EXPRESSION
FILE REFERENCE: ISPH-0607
CURRENT APPLICATION NUMBER: US/09/948,002
CURRENT FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: 09/661,753
PRIOR APPLICATION NUMBER: 09/661,753
PRIOR FILING DATE: 2000-09-14
PRIOR FILING DATE: 2000-09-17
NUMBER OF SEQ ID NOS: 71
SEQ ID NO 27
LENGTH: 1585
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Sequence 27, Application US/09948002; publication No. US20030050265A1; GENERAL INFORMATION:
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TCCTCATGGCCACCCCCTGGAAAGGGCTCAACACCTGCACAGCTCCAGGCACCGGAGA-
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                                                       CCCTGGATACCAACAGCTACCCATACGACGTGCCAGACTACGCATCTCTGGCCCTGGATA
                                                                                                              TCCTCATGGCCACCCCGCTGGAGAGGGGCCCAGCACCTGCACAGCTCCCGGGCACCGCCGAG
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; LOCATION: (1)..(1368)
US-09-756-283A-19
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US-09-756-283A-19
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SEQ ID NO 19
LENGTH: 1376
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                           Query Match
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APPLICANT: Dreja, Hanna Stina
APPLICANT: Adams, Gillian
TITLE OF INVENTION: Latent Fusion Protein
FILE REFERENCE: 0623,1000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
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                                            CTGACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG
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                                                                                                                                   AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT 250
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88.1%;
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Pred. No. 2.9e-167;
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US-09-756-283A-21
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APPLICANT: Dreja, Hanna Stina
APPLICANT: Adams, Gillian
TITLE OF INVENTION: Latent Fusion Protein
FILE REFERENCE: 0623.1000000
CURRENT APPLICATION NUMBER: US/09/756,283A
CURRENT FILING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 100
SOFTWARE: PatentIn version 3.0
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                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial
FEATURE:
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               CCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTTTA
                                             GAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTCGCCAG
                                                           GAAGCGGAAGCGCATCGAGGCCATTCGCGGGCCAGATTCTGTCCAAGCTTCGGCTTCGCCAG 192
                                                                                                      GGCGGGAGGGGCTCAGCGGCCGCACTATCCACCTGCAAGACTATCGACATGGAGCTGGT
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662;
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Similarity 87.0%;
                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                             Score 591.4; DB 10;
Pred. No. 2.4e-150;
0; Mismatches 96;
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US-09-813-271B-1
Sequence 1, Application US/09813271B; Patent No. US20020115834A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                373 TGATAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTCCG 432
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                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,271B
FILING DATE: 20-Mar-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (A) Nico Cerletti
TITLE OF INVENTION: New process for the production biologically active protein
                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAA 729
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                                                                                                                                                                                                                                                                                                                                                CITY: Summit
STATE: New Jersey
                                           APPLICATION NUMBER: PCT/EP95/02719 FILING DATE: 12-Jul-95
                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
APPLICATION NUMBER: EPO 94810439.3 FILING DATE: 25-Jul-94
                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: No. US20020115834Alartis Patent Department
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                                                                                                                                                                                                                                                                                                                                                                                           564 Morris Avenue
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US-10-028-158-20 ; Sequence 20, Application US/10028158 ; Patent No. US20020110833A1
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                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 320;
                                                                              CURRENT APPLICATION NUMBER: US/10/028,158
CURRENT FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: US/09/380,662
PRIOR FILING DATE: 1999-12-21
                                                                                                                                                               TITLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF TITLE OF INVENTION: TROPHOBLAST FILE REFERENCE: 11757.38USWO
                                                                                                                                                                                                                           APPLICANT: Caniggia, Isabella APPLICANT: Post, Martin APPLICANT: Lye, Stephen
PRIOR APPLICATION NUMBER: US 60/039,919
PRIOR FILING DATE: 1997-03-07
                                        PRIOR APPLICATION NUMBER: PCT/CA98/00180 PRIOR FILING DATE: 1998-03-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1196 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1136 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 1195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1016
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                                                                                                                                                                                                                                                                                                                                                                                                                                   301 CTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGA 339
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 522-6940
TELEFAX: (908) 522-6955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Pfeiffer, Hesna J. .
REGISTRATION NUMBER: 22640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
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Pred. No. 4.7e-74;
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; NAME/KEY: CDS
; LOCATION: (254)..(1492)
US-10-028-158-20
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SEQ ID NO 20
LENGTH: 2574
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Best Local
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nes 666; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTAAGCGGAATGAGCAGAGCATCGAGCTCTTCCAGATCCTTCGGCCAGATGAGCACATTG
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TCATGATGATTCCCCCCACACCGGCTCGACAACCCGGGCCAGGGGGGGTCAGAGGAAGAAGC
                                  GGCACCGCCGAGCCCTGGATACCAACAGCTACCCATACGACGTGCCAGACTACGCATCTC 893
                                                                       GTGGAGATCTGGGGCGCCT---CAAGAAGCAGAAGGATCACCACAACCCTCATCTAATCC
                                                                                                          GGCCCTTCCTGCTCATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCC 833
                                                                                                                                               ACATTCACGAGGTGATGGAAATCAAATTCAAAGGCGTGGACAATGAGGÄTGACCATGGCC
                                                                                                                                                                                 AAATTAACGGGTTCAATTCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACC
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                                                                                                                                                                                                                                                                                                CCTTTGATGTCACTGACACTGTGCGTGAGTGGCTGTTGAGAAGAGAGTCCAACTTAGGTC
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US-09-813-271B-7
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                                                                                                                                                           INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Pfeiffer, Hesna J.
REGISTRATION NUMBER: 22640
REFERENCE/DOCKET NUMBER: 4 20039C/ClCl/USN
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: New process for the production biologically active protein
                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/02719
FILING DATE: 12-Jul-95
APPLICATION NUMBER: EPO 94810439.3
FILING DATE: 25-Jul-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 07901
COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: No. US20020115834Alartis Patent Department
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              TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "recombinant hybrid DNA of
IMMEDIATE SOURCE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 564
CITY: Summit
                                                                                                LENGTH: 336 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                    TELEPHONE: (908) 522-6955
TELEFAX: (908) 522-6955
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/813,271B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: New Jersey
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coli LC137/pPLMu.TGF-beta1(44/45)beta3
                                                                                                                                                                                                                            (908) 522-6940
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US-09-813-271B-5
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                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/09813271B Patent No. US20020115834A1 GENERAL INFORMATION:
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SEQUENCE DESCRIPTION: SEQ ID NO: 7:
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             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,271B
FILING DATE: 20-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (A) Nico Cerletti
TITLE OF INVENTION: New process for the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 13
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PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: /product= "N-terminal 44 amino acids of human TGF-betal"
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LOCATION: 1..336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: /product= "hybrid TGF-beta named
                                                                                                                                                                                                                                   STREET: 564 Morris Avenue
                                                                                                                                                                                                                                                      ADDRESSEE: No. US20020115834Alartis Patent Department
                                                                                                                                                                                                STATE: New Jersey
                                                                                                                                                                                                                   CITY: Summit
                                                                                                                                                                               COUNTRY: USA
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                                                                                                                                                                                                                                                                                                         biologically active protein
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Best Local (
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SEQUENCE CHARACTERISTICS:
LENGTH: 339 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1196 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: cDNA to mRNA IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: /product= "human TGF-beta3"
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
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                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                               NUMBER OF SEQUENCES: 13
                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                      CTCTCCAACATGGTGGTGAAGTCTTGTAAATGTAGCTGA 339
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FILING DATE: 12-Jul-95
APPLICATION NUMBER: EPO 94810439.3
FILING DATE: 25-Jul-94
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLONE: E. coli LC137/pPLMu.hTGF-beta3 (DSM 5658)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (908) 522-6940
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                                       STATE: New Jersey
                                                           CITY: Summit
                                                                              STREET: 564 Morris Avenue
ZIP: 07901
                    COUNTRY: USA
                                                                                                ADDRESSEE: No. US20020115834Alartis Patent Department
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                                                                                                                                                                                               (A) Nico Cerletti
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                                                                                                                                                                           New process for the production
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301 CTTTCTAATATGATTGTAAAGTCTTGCAAATGCAGC 336

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US-09-813-271B-11
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                     1196 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGC 1231
                                                                                                                   1136 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 1195
                                                                                                                                                                                                                    1076 GTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGCGTCGCGGCGCGCGTGCTGCGTGCCG 1135
                                                                                                                                                                                                                                                                                                                     1016 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 1075
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                                                                 241 CAAGATTTAGAACCTCTAACCATTCTCTACTACATTGGCAAAACACCCCAAGATTGAACAG 300
                                                                                                                                                                     181 GTCCTGAGCTTATATAATACCATAAATCCAGAAGCATCTGCTTCTCCTTGCTGCGTGTCC 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: 1..336
OTHER INFORMATION: /product= "hybrid TGF-beta3-2"
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 22640
REFERENCE/DOCKET NUMBER: 4-20039C/C1C1/USN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 522-6940
TELEFAX: (908) 522-6955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,271B
FILING DATE: 20-Mar-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/02719
FILING DATE: 12-Jul-95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DESCRIPTION: /desc = "recombinant hybrid DNA IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 336 base pairs
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                                                                                                                                                                                                                                                                                                                                                                       TACATTGACTTCCGACAGGATCTGGGCTGGAAGTGGGTCCATGAACCTAAGGGCTACTAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: /product= "N-terminal 44 amino acids of human TGF-beta3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: /product= "C-terminal 68 amino acids of human TGF-beta2"
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: mat_peptide
LOCATION: 133..336
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OTHER INFORMATION: /product= "hybrid TGF-beta2-3" SEQUENCE DESCRIPTION: SEQ ID NO: 9: US-09-813-271B-9
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US-09-813-271B-9
                                                                                       Query Match
Best Local Similarity
                                                                        Matches 239;
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INFORMATION FOR SEQ ID NO: 9:
APPLICATION NUMBER: PCT/EP95/02719
FILING DATE: 12-Jul-95
APPLICATION NUMBER: EPO 94810439.3
FILING DATE: 25-Jul-94
ATTORNEY/AGENT INFORMATION:
NAME: Pfeiffer, Hesna J.
REGISTRATION NUMBER: 22640
REFERENCE/DOCKET NUMBER: 4-20039C/C1C1/USN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 522-6940
TELEFAX: (908) 522-6955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,271B
FILING DATE: 20-Mar-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DESCRIPTION: /desc = "recombinant hybrid DNA IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 336 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: New process for the production
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                                                                                                                                                                                                                                                                                                  NAME/KEY: mat_peptide LOCATION: 133..336 OTHER INFORMATION: /pro
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                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: mat_peptide LOCATION: 1..132
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STRANDEDNESS: double
                                                                                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                       acids of human TGF-beta2"
                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: /product= "N-terminal 44 amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLONE: E. coli LC137/pPLMu.TGF-beta2(44/45)beta3
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                                                                        Conservative
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71.1%;
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                                                                   Pred. No. 1.6e-39;
0; Mismatches 97;
                                                                                                          Score 180.8;
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; Sequence 47, Application US/09948002
; Publication No. US20030050265A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 47
LENGTH: 4267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/948,002
CURRENT FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: 09/661,753
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/154,546
PRIOR FILING DATE: 1999-09-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Nicholas M. Dean
APPLICANT: Susan F. Murray
TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
TITLE OF INVENTION: FACTOR BETA EXPRESSION
FILE REFERENCE: ISPH-0607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Mus musculus FEATURE:
NAME/KEY: CDS
LOCATION: (1218)...(2462)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
1486 AGCGCGAGCGAGCGAGCAGGAGTACTACGCCAAGGAGGTTTATAAAATCGACATGCCGT 1545
                                                                                                                                                                                           1369
                                                                                                                                                                                                                                                                      1309 AGTTTATGCGCAAGAGGATCGAGGCCATCCGGGGCAGATCCTGAGCAAGCTGAAGCTCA 1368
                                                                                                                                                                                                                                                                                                                                                              1249 TCCTGCATCTGGTCCCGGTGGCGCTCAGTCTGTCTACCTGCAGCACCCTCGACATGGATC 1308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1196 CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGC 1231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1136 CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 1195
                                                        297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 CTCTCCAACATGGTGGTGAAGTCTTGTAAATGTAGC 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 GTGCTGGGACTGTACAACACTCTGAACCCTGAAGCATCTGCCTCGCCTTGCTGCGTGCCC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 CAGGACCTGGACCCCTGACCATCCTGTACTATGTTGGGAGGACCCCCAAAGTGGAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    956 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCCAAGGGCTACCAT 1015
                                                                                                                                                                                                                                                                                                                                                                                        69 TGCTGACGCCTGGCCGGCCGGCCGGCCGGCCGGCCTGCCACCTGCAAGACCATCGAACATAGAAC 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 13.2%;
Local Similarity 51.9%;
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                                                                                                                                                                                                                         CCAGCCCCCGAGCCAGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTC 248
                                                                                                                                                                                                                                                                                                TGGTGAAGCGGAAGCGCATCGAGGCCATTCGCGGGCCAGATTCTGTCCAAGCTTCGGCTTG 188
                                               AGCCCGAGCCAGAGGCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAA 356
                                                                                         TCTACAACAGTACCAGGGACTTACTGCAGGAGGAAGGCAAGCCGGAGGGCAGCCGCCTGCG 1485
                                                                                                                               TTTACAACAGTACCCGCGAC-----CGGGTAGCCGGGGAAAGTGTCGAACCGG 296
                                                                                                                                                                                 CCAGCCCCCG---GAAGACTATCCGGAGCCGGATGAGGTCCCCCCGGAGGTGATTTCCA 1425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGCGTCGGCGGCGGCGGCGTGCCGTGCCG 1135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTTTGGATGCGGCCTATTGCTTTAGAAATGTGCAGGATAATTGCTGCCTACGTCCACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 532; Indels 56; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 179.8; DB 9; Pred. No. 5.4e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 4267;
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                                1217 TCCTGCAAGTGCAGCTGAGGCCC 1239
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                                                                                                                                                                                                                                                2145 TTTAGAAATGTGCAGGATAATTGCTGCCTTCGCCCTCTTTACATTGATTTTAAGAGGGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1786 TGAAAACCAGAGCGGAGGGTGAATGGCTCTCCTTCGACGTGACAGACGCTGTGCAGGAGT 1845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2086 GACTGGAGTCACAACAGTCCAĢCCGGCGGAAGA-AGCGCGCTTTGGATGCTGCCTACTGC 2144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2026 CTAGGAAAAAACCAGTGGGAAGACCCCACATCTCCTGCTAATGTTGTTGCCCTCCTACA 2085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1966 TIGCAGGTATTGATGGCACCTCTACATATGCCAGTGGTGATCAGAAAACTATAAAGTCCA 2025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1906 CCTTCGTGCCGTCTAATAATTACATCATCCCGAATAAAAGCGAAGAGCTCGAGGCGAGAT 1965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1726 AGATCCTTAAATCCAAAGACTTAACATCTCCCACCCAGCGCTACATCGATAGCAAGGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          917 TTCAGCTCCACGGAGAACAACTGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGAC 976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   857 AACAGCTACCCATACGACGTGCCAGACTACGCATCTCTGGCCCTGGATACCAACTACTGC 916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     798 CCCCGCTGGAGAGGGCCCAGCA-CCTGCACAGCTCCCGGCACCGCCGAGCCCTGGATACC 856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      738 GCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTCCTCATGGCCA 797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             690 GC-----AAAGATAACACACTCCACGTGGAAATTAACGGGTTCAATTCTGGCC 737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              630 GCCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCCTCAGTGCCCACTCTTCCTCTGACA 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        570 TGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTCACCGGAGTTGTGCGGCAGT 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   357 GCGGCAACCAAATCTATGATAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCA 416
                                                                                                                                                                                                                                                                                                                                 TGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAG 1096
                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCC 1036
TCTTGTAAATGCAGCTAAAGTCC 2467
                                                                                              ATTCTCTATTACATTGGAAATACGCCCAAGATCGAACAGCTTTCCAATATGATTGTCAAG 2444
                                                                                                                         ATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGT 1216
                                                                                                                                                                                                ATAAATCCCGAAGCTTCCGCTTCCCCTTGCTGTGTGTCCCAGGATCTGGAACCACTGACC
                                                                                                                                                                                                                                                                                                    TGCCCATATCTATGGAGTTCAGACACTCAACACACCAAAGTCCTCAGCCTGTACAACACC 2324
                                                                                                                                                                                                                                                                                                                                                                                                             CTTGGATGGAAATGGATCCATGAACCCAAAGGGTACAATGCTAACTTCTGTGCTGGGGGCA
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US-09-813-271B-3

Sequence 3, Application US/09813271B Patent No. US20020115834A1 GENERAL INFORMATION:

TITLE OF INVENTION:

New process for the production

(A) Nico

Cerletti

APPLICANT:

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US-09-813-271B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                    1076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/EP95/02719
FILING DATE: 12-Jul-95
APPLICATION NUMBER: EPO 94810439.3
FILING DATE: 25-Jul-94
ATTORNEY/AGENT INFORMATION:
NAME: Pfeiffer, Hesna J.
REGISTRATION NUMBER: 22640
REFERENCE/DOCKET NUMBER: 4-20039C/C1C1/USN
TELEPHONE: (908) 522-6940
TELEPHONE: (908) 522-6940
                                                                                                                                                                                                                                                                                                       1016
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                                                                                                                                                                                                                                                                                                                                                                       956 TACATTGACTICCGGAAGGACCIGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCAT 1015
                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
les 226; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GCTTTGGATGCGGCCTATTGCTTTAGAAATGTGCAGGATAATTGCTGCCTACGTCCACTT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,271B
FILING DATE: 20-Mar-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: No. US20020115834Alartis Patent Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE DESCRIPTION: SEQ ID NO: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: cDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 339 base pairs
                                                                                                                           CAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAG 1195
                                                                                                                                                                    GTCCTGAGCTTATATAATACCATAAATCCAGAAGCATCTGCTTCTCCTTGCTGCGTGTCC
                                                                                                                                                                                                              GTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGCGTCGGGGGGCGCGTGCTGCGTGCCG 1135
CTTTCTAATATGATTGTAAAGTCTTGCAAATGCAGCTAA 339
                                      CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1234
                                                                                    CAAGATTTAGAACCTCTAACCATTCTCTACTACATTGGCAAAACACCCCAAGATTGAACAG
                                                                                                                                                                                                                                                              GCCAACTTCTGTGCTGGAGCATGCCCGTATTTATGGAGTTCAGACACTCAGCACACCAGCAG
                                                                                                                                                                                                                                                                                                     GCCAATTTCTGCCTGGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG
                                                                                                                                                                                                                                                                                                                                                TACATTGATTTCAAGAGGGATCTAGGGTGGAAATGGATACACGAACCCAAAGGGTACAAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: New Jersey
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: 1..336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 158.2; DB 10;
Pred. No. 2.1e-33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "human TGF-beta2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 339;
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RESULT 14
US-10-044-090-323
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APPLICANT: O19a Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REFERENCE: PA-0028 US
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SEQ ID NO 323
LENGTH: 2912
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                APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-x-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 03/632,366
PRIOR APPLICATION NUMBER: US 03/632,366
PRIOR APPLICATION NUMBER: US 03/632,366
                                                                                                                                                                                                                                                                                                     APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R. APPLICANT: Hanzel, David K.
                                                                                                                                                                                                                                                                                  APPLICANT:
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Pred. No. 3.4e-33;
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Search completed: April 15, 2003, 11:57:16 Job time: 206 secs
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.9

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6.5

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6.5

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 7.8

US-09-864-761-15319
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 15319

LENGTH: 597

TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity 91.58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
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PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
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PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00661
FILING DATE: 2001-01-30
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FILING DATE: 2000-09-27
APPLICATION NUMBER: PCT/US01/00666
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Pred. No. 7.3e-29;
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Maximum DB seq length: 2000000000
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Perfect score:
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         703.6
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AGEN	mab32f06	01-E-E-0	UI-R-FF0		AGENCOUR	UI-H-DH1	G :	AGENCOUR	UI-H-EZ	DKFZp434B	BOTL01	BM974192 UT-CF-EC1	BM917472 AGENCOURT	BE311897 601142424	BI905963 603062849	BE615330 601280728	BG68384	AI743724 wq53b06.x	BG500488 602544826	BM802192 AGENCOURT	BO672677 AGENCOURT	BM068788 ie85a02.v	BI686959 603313837	BF682938 602117568	BG938856 cn28q07.v	AI148173 gb56d01.x	AI131171 qc15c11.x	BE261764 601147839	BO053417 AGENCOURT	BI195242 602944518	BG748049 602705544	BI909079 603070060	AGENCOL	2 3	0952138 AGENCO	AL530080	6028697	603037

ALIGNMENTS

FEATURES Fissue Procurement: Life Technologie cDNA Library Preparation: Life Technologie cDNA Library Preparation: Life Technologie cDNA Library Arrayed by: The I.M.A. A. DNA Sequencing by: Agencourt Biosci Clone distribution: MGC clone distribu	ĄL		Eukaryota; Metazoa; (Mammalia; Eutheria; REFERENCE 1 (bases 1 to 1072)	ORGANISM Homo sapiens	DS	ACCESSION BM562135 TVERSION BM562135.1 GI:18807966	BM562135 LOCUS LOCUS BM562135 LOCUS DEFINITION AGENCOURT_6562032 t 5', mRNA sequence.
Tissue Procurement: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM12768 row: h column: 08 High quality sequence start: 9 High quality sequence stop: 647. Location/Qualifiers	ausberg, Ph.D.	NIH-MGC http://mgc.nci.nih.gov/.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1072)			7966	BM552135 BM562135 BM562135 TIPM TOTAL BHOMO SAPIENS CDNA CLONE IMAGE:5745463 S', mRNA sequence.

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                                                                                                                                                                                                                                                                                                                                                                                                                            CAGTGCCCACTCTTCCTCTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTT
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           CCTGGATACCAACAGCTACCCATACGACGTGCCAGACTACGCATCTCTGGCCCTGGATAC
                                         TCTCATGGCCACCCCGCTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGCCACCGCCGAGC
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/clone="IMAGE:5745463"
/clone_lib="NIH_MGC_118"
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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Conservative
                                                                                                         /clone_lib="NIH MGC_88"
/tissue_type="duodenal adenocarcinoma, cell line"
/tissue_type="duodenal adenocarcinoma, cell line"
/lab_host="DH108 (phage-resistant)"
/note="Organ: small intestine; Vector: pcMV-SPORT6;
/note="Organ: small intestine; Vector: pcMV-SPORT6;
/note="Organ: small intestine; Vector: pcMV-SPORT6;
/site_1: Note: Sall; Cloned unidirectionally;
/oligo-dT primed. Average insort size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC Library."

a 329 c 345 g 154 t 13 others
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/db_xref="taxon:9606"
                       44.6%;
80.9%;
                       Score 607; DB 13;
Pred. No. 2.6e-122;
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                                                         AGCTCCGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGA
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1 (bases 1 to 789)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seqref@genoscope.cns.fr, Web : www.genoscope.cns.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com" 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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                        AGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTCGCCAGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plate: LLCM195 row: h column: 17
High quality sequence start: 2
High quality sequence stop: 713.
Location/Qualifiers
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Tissue Procurement: ATCC
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National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
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                                                                                                                                                                                                                                               /clone="IMAGE:3510592"
/clone=libe"NIH_MGC_19"
/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
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                                                                        CDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LICM193 row: m column: 04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
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                                                                                                                                                                                                                                    Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                    Unpublished (1999)
Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                        NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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1 (bases 1 to 717)
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                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
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/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: brain; Vector: pOTB7; Site_1: xhoI; Site_2: ECORI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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516 AGCTATACCAGAAATACAGCAATGATTCCTGGCGCTACCTCAGCAACCGGCTGCTGGCCC
                                              301 TGCTCTCCCGGGCAGAGCTGCGTCTGCTGAGGCTCAAGTTAAAAGTGGAGCAGCAGCAGGGGG
                                                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 216 CGCCCGGCCGCTGCCTGAGGCAGTACTGGCTCTTTACAACAGTACCGCGACCGGGTAG 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156 TTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCCAGCCCCCCGAGCCAGGGGGACGTGC 215
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                                                                                            TGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTCAAGTTAAAAGTGGAGCAGCACGTGG 515
                                                                                                                                          ACAGCATATATATGTTCTTCAACACATCAGAGCTCCGAGAAGCGGTACCTGAACCCGTGT 300
                                                                                                                                                                                        ACAGCTTATATATGCTGTTCAACACGTCGGAAGCTCCGGGAAGCGGTGCCGGAACCTGTAT 455
                                                                                                                                                                                                                                         CCCGCGTGCTAATGGTGGAAACCCACAACGAAATCTATGACAAGTTCAAGCAGAGTACAC
                                                                                                                                                                                                                                                                                       CCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATCTATGATAAATTCAAGGGCACCCCCC 395
                                                                                                                                                                                                                                                                                                                                           CCGGGGAGAGTGCAGAACCGGAGCCCGAGCCTGAGGCCGACTACTACGCCAAGGAGGTCA
                                                                                                                                                                                                                                                                                                                                                                  CCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAGGCGGACTACTACGCCAAGGAGGTCA 335
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plate: LLCM2375 row: c column:
High quality sequence stop: 599
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BQ675698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC http://mgc.nci.nih.gov/.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="epidermoid carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAGCAG(G). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-cDNA
synthesis kit (Stratagene) and Superscript II RT (Life
Technologies). Note: this is a NHE_MGC Library."
a 292 c 255 g 161 t
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86.7%;
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BI818841.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
Contact: Robert St:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plate: LLAM11444 row: n column: High quality sequence stop: 874.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
                     Similarity
                                                                                                   170
Conservative
                                                                                          /note="Organ: pooled brain, lung, testis; Vector: /note="Organ: pooled brain, lung, testis; Vector: pcMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; land lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                         /clone_lib="NIH_MGC_115"
                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
/clone="IMAGE:5178433"
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                   39.3%;
87.2%;
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  0;
                   Score 534.4; DB 13; Pred. No. 1.8e-106;
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                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 956)
                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                    mRNA sequence.
BI084718
                                                      Tissue Procurement: ATCC
                                                                 Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                            Unpublished (1999)
                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
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cDNA Library Preparation: CLONETECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
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                                                  TCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTGTACATTGACTTCCGCAAGGACC
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                                                                                              TCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="epidermoid carcinoma, cell line"
/lab_host="DH10B (phage resistant)"
/note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-cDNA
synthesis kit (Stratagene) and Superscript II RT (Life
Technologies). Note: this is a NIH_MGC Library."
a 273 c 312 g 199 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
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BP 191 91006 EVRY cedex - France
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: segref@genoscope.cns.fr,
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                                                                                                                                                                              142
                                                                              Conservative
                                                                                                                                                                            D
                                                                                                                                                                                                        /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email fliang@lifetech.com URL:
                                                                                                                                                                          http://fulllength.invitrogen.com"
228 c 274 g 145 t
                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="neuroblastoma cells"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="CSODD009YM06"
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                                                                                                                                                                                                                                                                                              Email:
Tissue
                          Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 871)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                    BQ952138
BQ952138.1 GI:22367616
EST.
                                                                                                                                                                                    871 bp mRNA linear EST AGENCOURT_8948622 NCI_CGAP_CO24 Mus musculus cDNA clone IMAGE:6478644 5', mRNA sequence.
                                                                                                                          Mus musculus
                                                                                                                                          house mouse.
              cgapbs-r@mail.nih.gov
 Procurement: The Cepko Laboratory
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                                            ACGTCACTGGAGTTGTACGGCAGTGGCTGAACCAAGGAGACGGAATACAGGGCTTTCGAT
                                                                                                             GGCGTTACCTTGGTAACCGGCTGCTGACCCCCACTGATACGCCTGAGTGGCTGTCTTTTG
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Plate: LLAM14022 row:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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//lab_host="DH10B (Tl phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Not1;
/note="Organ: colon; Vector: pCMV-SPORT6; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
/rechnologies. Note: this is a NCI_CGAP Library."

a 283 c 237 g 148 t 4 others
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/db_xref="taxon:10090"
/clone="IMAGE:6478644"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1013)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Plate: LLAM12265 row:
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                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="NH_MGC_85"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lymph; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.867 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NHL_MGC Library."

a 333 c 291 g 163 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5551510"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Daniel McVicar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
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Plate: LLCM2125 row: k column:
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National Institutes of Health, Mammalian
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
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Location/Qualifiers
                /note="Organ: blood; Vector: pOTB7; Site_1: XhoI; Site_2: ECORI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the Laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
                                                                                                                                                                              /tissue_type="natural killer cells, cell line"
/lab_host="DH10B (phage-resistant)"
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/clone_lib="NIH_MGC_106"
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/db_xref="taxon:9606"
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Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 943)
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Location/Qualifiers
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Contact: Robert Strausberg, Ph.D
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National Institutes of Health, Mammalian
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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/db_xref="taxon:9606"
/clone="IMAGE:5218983"
/clone_lib="NIH_MGC_118"
/tissue_type="leukocyte"
/lab_host="DH108"
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315 c 291 g 166 t 1 others
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1 (bases 1 to 821)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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High quality sequence stop: 812.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tissue Procurement: ATCC
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    /Clone_lib="NIH_MCC_43"
//Lissue_type="normal pigmented retinal epithelium"
//Lissue_type="normal pigmented retinal epithelium"
//Lab_most="DH10B (phage-resistant)"
//note="079an: eye; Vector: pOTB7; Site_1: XhoI; Site_2: ECORI; CNA made by oligo-dT priming. Directionally cloned into ECORI/XhoI sites using the following 5; adaptor: GCCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MCC Library. | "
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                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
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Query Match

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                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 773)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GOCTGCTGAGGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCA 536
                                                                                                                                                                                                                                                                                                                                                                                                                                     TGTCCTTTGATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGG 656
                                                                                                                                                                    ATTAACGGGTTCAATTCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGG 775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGATTCCTGGCGCTACCTCAGCAACCGGCTGCTGCTCGCCCCCAGTGACTCACCGGAGTGGC 596
                                                                                                                                                                                                                                                                                         GCTTTCGCCTTAGACGCCCACTAGTCCTGTGACAGCAGGGAT-ACACACTGCAAGTGGAC 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 708.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183
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/Clone_1ib="NIH_MGC_19"
/clone_1ib="NIH_MGC_19"
/tissue_type="neuroblastoma"
/tissue_type="neuroblastoma"
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/note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
/note: togan: brain; Vector: pOTB7; Site_1: XhoI; Site_2: Xh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36.9%;
83.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 501.8; DB 13; Length 773; pred. No. 2.2e-99; 0; Mismatches 117; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Db 719 CGGAACCGCCGAGCCATGGACACCAGCAATTGC 751

Search completed: April 15, 2003, 11:52:21 Job time: 2239 secs